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OM protein - protein search, using sw model

Run on: February 10, 2005, 17:39:57 ; Search time 476 Seconds
(without alignments)
912.812 Million cell updates/sec

Title: US-09-892-287-1
Perfect score: 2020
Sequence: 1 MDVLSPLSFIKVSVMQGI.....FQIPPGSLREDPLGEAQPQI 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|--------|------------|--------|----|----------------------|-------------------|
| | | Match | Length | | | |
| 1 | 2020 | 100.0 | 372 | 23 | US-09-892-287-1 | Sequence 1, Appli |
| 2 | 2020 | 100.0 | 372 | 35 | US-10-990-328-8797 | Sequence 8797, Ap |
| 3 | 2020 | 100.0 | 448 | 1 | PCT-US02-17526-14 | Sequence 14, Appl |
| 4 | 2020 | 100.0 | 448 | 27 | US-10-161-510-14 | Sequence 14, Appl |
| 5 | 2020 | 100.0 | 448 | 35 | US-10-990-328-8795 | Sequence 8795, Ap |
| 6 | 2020 | 100.0 | 448 | 35 | US-10-990-328-8796 | Sequence 8796, Ap |
| 7 | 2020 | 100.0 | 449 | 27 | US-10-170-205E-32368 | Sequence 32368, A |
| 8 | 2020 | 100.0 | 449 | 35 | US-10-990-328-8794 | Sequence 8794, Ap |
| 9 | 2020 | 100.0 | 480 | 21 | US-09-724-676-79765 | Sequence 79765, A |
| 10 | 2020 | 100.0 | 480 | 21 | US-09-724-676-79776 | Sequence 79776, A |
| 11 | 2020 | 100.0 | 480 | 21 | US-09-724-676-79782 | Sequence 79782, A |
| 12 | 2020 | 100.0 | 480 | 21 | US-09-724-676A-79765 | Sequence 79765, A |
| 13 | 2020 | 100.0 | 480 | 21 | US-09-724-676A-79776 | Sequence 79776, A |
| 14 | 2020 | 100.0 | 480 | 21 | US-09-724-676A-79782 | Sequence 79782, A |
| 15 | 2012 | 99.6 | 478 | 1 | PCT-US02-17526-11 | Sequence 11, Appl |
| 16 | 2012 | 99.6 | 478 | 27 | US-10-161-510-11 | Sequence 11, Appl |
| 17 | 2010 | 99.5 | 372 | 1 | PCT-US02-17382-158 | Sequence 158, App |
| 18 | 2010 | 99.5 | 372 | 1 | PCT-US02-17526-13 | Sequence 13, Appl |
| 19 | 2010 | 99.5 | 372 | 27 | US-10-161-510-13 | Sequence 13, Appl |
| 20 | 2010 | 99.5 | 448 | 1 | PCT-US02-17526-12 | Sequence 12, Appl |
| 21 | 2010 | 99.5 | 448 | 27 | US-10-161-510-12 | Sequence 12, Appl |
| 22 | 1991 | 98.6 | 518 | 21 | US-09-724-676-79769 | Sequence 79769, A |
| 23 | 1991 | 98.6 | 518 | 21 | US-09-724-676-79770 | Sequence 79770, A |
| 24 | 1991 | 98.6 | 518 | 21 | US-09-724-676-79771 | Sequence 79771, A |
| 25 | 1991 | 98.6 | 518 | 21 | US-09-724-676A-79769 | Sequence 79769, A |
| 26 | 1991 | 98.6 | 518 | 21 | US-09-724-676A-79770 | Sequence 79770, A |
| 27 | 1991 | 98.6 | 518 | 21 | US-09-724-676A-79771 | Sequence 79771, A |
| 28 | 1984 | 98.2 | 532 | 21 | US-09-724-676-79783 | Sequence 79783, A |
| 29 | 1984 | 98.2 | 532 | 21 | US-09-724-676-79784 | Sequence 79784, A |
| 30 | 1984 | 98.2 | 532 | 21 | US-09-724-676-79785 | Sequence 79785, A |
| 31 | 1984 | 98.2 | 532 | 21 | US-09-724-676A-79783 | Sequence 79783, A |
| 32 | 1984 | 98.2 | 532 | 21 | US-09-724-676A-79784 | Sequence 79784, A |
| 33 | 1984 | 98.2 | 532 | 21 | US-09-724-676A-79785 | Sequence 79785, A |
| 34 | 1966.5 | 97.4 | 565 | 21 | US-09-724-676-79786 | Sequence 79786, A |
| 35 | 1966.5 | 97.4 | 565 | 21 | US-09-724-676-79787 | Sequence 79787, A |
| 36 | 1966.5 | 97.4 | 565 | 21 | US-09-724-676-79788 | Sequence 79788, A |
| 37 | 1966.5 | 97.4 | 565 | 21 | US-09-724-676A-79786 | Sequence 79786, A |

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| 38 | 1966.5 | 97.4 | 565 | 21 | US-09-724-676A-79787 | Sequence 79787, A |
| 39 | 1966.5 | 97.4 | 565 | 21 | US-09-724-676A-79788 | Sequence 79788, A |
| 40 | 1955 | 96.8 | 570 | 21 | US-09-724-676-79772 | Sequence 79772, A |
| 41 | 1955 | 96.8 | 570 | 21 | US-09-724-676-79773 | Sequence 79773, A |
| 42 | 1955 | 96.8 | 570 | 21 | US-09-724-676-79774 | Sequence 79774, A |
| 43 | 1955 | 96.8 | 570 | 21 | US-09-724-676A-79772 | Sequence 79772, A |
| 44 | 1955 | 96.8 | 570 | 21 | US-09-724-676A-79773 | Sequence 79773, A |
| 45 | 1955 | 96.8 | 570 | 21 | US-09-724-676A-79774 | Sequence 79774, A |

ALIGNMENTS

RESULT 1

US-09-892-287-1

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; Sequence 1, Application US/09892287
; GENERAL INFORMATION:
;   APPLICANT: Hillman, Jennifer L.
;             Lal, Preeti
;             Corley, Neil C.
;             Shah, Purvi
;   TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL
;                       (4,5) BISPHOSPHATE 5-PHOSPHATASE
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Drive
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/892,287
;     FILING DATE: 26-Jun-2001
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 09/258,643
;     FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Billings, Lucy J.
;     REGISTRATION NUMBER: 36,749
;     REFERENCE/DOCKET NUMBER: PF-0334 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-855-0555
;     TELEFAX: 415-845-4166
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 372 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;     LIBRARY: BRSTNOT03
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; CLONE: 638789
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-892-287-1

Query Match 100.0%; Score 2020; DB 23; Length 372;
Best Local Similarity 100.0%; Pred. No. 6.7e-198;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    361 REDPLGEAQPQI 372
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RESULT 2
US-10-990-328-8797
; Sequence 8797, Application US/10990328
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8797
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-990-328-8797

Query Match 100.0%; Score 2020; DB 35; Length 372;

Best Local Similarity 100.0%; Pred. No. 6.7e-198;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

PCT-US02-17526-14

; Sequence 14, Application PC/TUS0217526

; GENERAL INFORMATION:

; APPLICANT: EXELIXIS, INC.

; TITLE OF INVENTION: PIBs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

; FILE REFERENCE: EX02-074C-PC

; CURRENT APPLICATION NUMBER: PCT/US02/17526

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US 60/296,076

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/328,605

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/357,253

; PRIOR FILING DATE: 2002-02-15

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US02-17526-14

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Best Local Similarity 100.0%; Pred. No. 8.9e-198;

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| Db | 257 | DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 316 |
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| | | | |
| Db | 317 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY | 376 |
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| | | | |
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| Db | 437 | REDPLGEAQPQI | 448 |

RESULT 4

US-10-161-510-14

; Sequence 14, Application US/10161510

; GENERAL INFORMATION:

; APPLICANT: EXELIXIS, INC.

; TITLE OF INVENTION: PIBs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

; FILE REFERENCE: EX02-074C

; CURRENT APPLICATION NUMBER: US/10/161,510

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US 60/296,076

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/328,605

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/357,253

; PRIOR FILING DATE: 2002-02-15

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-161-510-14

Query Match 100.0%; Score 2020; DB 27; Length 448;

Best Local Similarity 100.0%; Pred. No. 8.9e-198;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Db | 77 | MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL | 136 |
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| Qy | 61 | KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 120 |
| | | | |
| Db | 137 | KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 196 |
| | | | |
| Qy | 121 | IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY | 180 |
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| Db | 197 | IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY | 256 |
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| Qy | 181 | DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 240 |
| | | | |
| Db | 257 | DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 316 |
| | | | |
| Qy | 241 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY | 300 |
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| Db | 317 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY | 376 |
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| Qy | 301 | VSYAWVGDSKVSCLNQLNQYIDISNIPTTEDEFLLCYYSNLSRSVVGISRPFQIPPGSL | 360 |
| | | | |
| Db | 377 | VSYAWVGDSKVSCLNQLNQYIDISNIPTTEDEFLLCYYSNLSRSVVGISRPFQIPPGSL | 436 |
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| Qy | 361 | REDPLGEAQPQI | 372 |
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| Db | 437 | REDPLGEAQPQI | 448 |

RESULT 5

US-10-990-328-8795

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; Sequence 8795, Application US/10990328
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8795
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-990-328-8795
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Query Match          100.0%; Score 2020; DB 35; Length 448;
Best Local Similarity 100.0%; Pred. No. 8.9e-198;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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| Qy | 1 | MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL | 60 |
| | | | |
| Db | 77 | MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL | 136 |

Qy 61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
 |||
 Db 137 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 196

Qy 121 IEDFGLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
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 Db 197 IEDFGLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLLPPTYKFDRNSNDY 256

Qy 181 DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
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 Db 257 DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 316

Qy 241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVNDY 300
 |||
 Db 317 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVNDY 376

Qy 301 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFIIPGSL 360
 |||
 Db 377 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFIIPGSL 436

Qy 361 REDPLGEAQPQI 372
 |||
 Db 437 REDPLGEAQPQI 448

RESULT 6

US-10-990-328-8796

; Sequence 8796, Application US/10990328

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES

; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CL001495

; CURRENT APPLICATION NUMBER: US/10/990,328

; CURRENT FILING DATE: 2004-11-17

; NUMBER OF SEQ ID NOS: 558824

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 8796

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-990-328-8796

Query Match 100.0%; Score 2020; DB 35; Length 448;

Best Local Similarity 100.0%; Pred. No. 6.9e-198;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQLSTKSTPTGLFGYWGNGGGVNICL 60
 |||
 Db 77 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQLSTKSTPTGLFGYWGNGGGVNICL 136

Qy 61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
 |||
 Db 137 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 196

Qy 121 IEDFGLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180


```

Db      197  |||||
            IEDFGLHFVRESIKNRCYGGWLEKDQLSIKKHDPDLLREFQEGRLLPPTYKFDRNSNDY 256

Qy      181  DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
            |||||

Db      257  DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 316

Qy      241  TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
            |||||

Db      317  TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 376

Qy      301  VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLSRVVGISRPFQIPPGSL 360
            |||||

Db      377  VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLSRVVGISRPFQIPPGSL 436

Qy      361  REDPLGEAQPQI 372
            |||||

Db      437  REDPLGEAQPQI 448

```

RESULT 7

US-10-170-205E-32368

; Sequence 32368, Application US/10170205E

; GENERAL INFORMATION:

; APPLICANT: ADAMS, Mark

; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN

; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF

; FILE REFERENCE: CL001381

; CURRENT APPLICATION NUMBER: US/10/170,205E

; CURRENT FILING DATE: 2002-06-13

; NUMBER OF SEQ ID NOS: 40312

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 32368

; LENGTH: 449

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-170-205E-32368

```

Query Match          100.0%;  Score 2020;  DB 27;  Length 449;
Best Local Similarity 100.0%;  Pred. No. 8.9e-198;
Matches 372;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1  MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGGGVNICL 60
            |||||

Db      78  MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGGGVNICL 137

Qy      61  KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
            |||||

Db      138 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 197

Qy      121 IEDFGLHFVRESIKNRCYGGWLEKDQLSIKKHDPDLLREFQEGRLLPPTYKFDRNSNDY 180
            |||||

Db      198 IEDFGLHFVRESIKNRCYGGWLEKDQLSIKKHDPDLLREFQEGRLLPPTYKFDRNSNDY 257

Qy      181 DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
            |||||

```

```

Db      258 DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 317
Qy      241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      318 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 377
Qy      301 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      378 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 437
Qy      361 REDPLGEAQPQI 372
        ||||||||||||
Db      438 REDPLGEAQPQI 449

```

RESULT 8

US-10-990-328-8794

; Sequence 8794, Application US/10990328

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES

; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CL001495

; CURRENT APPLICATION NUMBER: US/10/990,328

; CURRENT FILING DATE: 2004-11-17

; NUMBER OF SEQ ID NOS: 558824

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 8794

; LENGTH: 449

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-990-328-8794

```

Query Match          100.0%;  Score 2020;  DB 35;  Length 449;
Best Local Similarity 100.0%;  Pred. No. 8.9e-198;
Matches 372;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGKGGVNICL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGKGGVNICL 137
Qy      61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      138 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 197
Qy      121 IEDFGLHFVRESIKNRCYGGLWEKDQLSIAKKHDPLLREFQEGRLLFPPPTYKFDRNSNDY 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      198 IEDFGLHFVRESIKNRCYGGLWEKDQLSIAKKHDPLLREFQEGRLLFPPPTYKFDRNSNDY 257
Qy      181 DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      258 DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 317
Qy      241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      318 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 377

```

```

Qy      301 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      378 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 437

Qy      361 REDPLGEAQPQI 372
        ||||||||||||
Db      438 REDPLGEAQPQI 449

```

RESULT 9

```

US-09-724-676-79765
; Sequence 79765, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79765
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-79765

```

```

Query Match          100.0%; Score 2020; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 9.9e-198;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGKGGVNICL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     109 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGKGGVNICL 168

Qy     61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCESGRDIPNILDHDLIIWFGDMNFR 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     169 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCESGRDIPNILDHDLIIWFGDMNFR 228

Qy    121 IEDFGLHFVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 IEDFGLHFVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 288

Qy    181 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    289 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 348

Qy    241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPDWIGLYKVGLRDVNDY 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPDWIGLYKVGLRDVNDY 408

Qy    301 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    409 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 468

Qy    361 REDPLGEAQPQI 372
        ||||||||||||

```

Db 469 REDPLGEAQPQI 480

RESULT 10

US-09-724-676-79776

; Sequence 79776, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79776
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-79776

Query Match 100.0%; Score 2020; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 9.9e-198;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWCNKGGVNICL 60
      |||
Db     109 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWCNKGGVNICL 168

Qy     61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
      |||
Db     169 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 228

Qy    121 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
      |||
Db    229 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 288

Qy    181 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
      |||
Db    289 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 348

Qy    241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
      |||
Db    349 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY 408

Qy    301 VSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 360
      |||
Db    409 VSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 468

Qy    361 REDPLGEAQPQI 372
      |||
Db    469 REDPLGEAQPQI 480
```

RESULT 11

US-09-724-676-79782

; Sequence 79782, Application US/09724676
; GENERAL INFORMATION:

; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79782
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-79782

Query Match 100.0%; Score 2020; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 9.9e-198;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      109 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 168

Qy      61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      169 KLYGYYVSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDIPNILDHDLIIWFGDMNFR 228

Qy     121 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLFPPTYKFDRNSNDY 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     229 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLFPPTYKFDRNSNDY 288

Qy     191 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     289 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 348

Qy     241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     349 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 408

Qy     301 VSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNSLSRVVGISRPFQIPPGSL 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     409 VSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNSLSRVVGISRPFQIPPGSL 468

Qy     361 REDPLGEAQPQI 372
          ||||||||||||
Db     469 REDPLGEAQPQI 480
```

RESULT 12
US-09-724-676A-79765
; Sequence 79765, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 79765
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-79765

Query Match 100.0%; Score 2020; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 9.9e-198;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGKGGVNICL 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     109 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGKGGVNICL 168

Qy     61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     169 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 228

Qy    121 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 288

Qy    181 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    289 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 348

Qy    241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY 408

Qy    301 VSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNLSRSVVGISRPFQIPPGSL 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    409 VSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNLSRSVVGISRPFQIPPGSL 468

Qy    361 REDPLGEAQPQI 372
      ||||||||||||
Db    469 REDPLGEAQPQI 480
```

RESULT 13

US-09-724-676A-79776
; Sequence 79776, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79776
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-79776

Query Match 100.0%; Score 2020; DB 21; Length 480;

Best Local Similarity 100.0%; Pred. No. 9.9e-198;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 60
      |||
Db     109 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 168

Qy     61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
      |||
Db     169 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 228

Qy    121 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
      |||
Db    229 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 288

Qy    181 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
      |||
Db    289 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 348

Qy    241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
      |||
Db    349 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 408

Qy    301 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 360
      |||
Db    409 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 468

Qy    361 REDPLGEAQPQI 372
      |||
Db    469 REDPLGEAQPQI 480
```

RESULT 14

US-09-724-676A-79782

; Sequence 79782, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 79782

; LENGTH: 480

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-676A-79782

Query Match 100.0%; Score 2020; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 9.9e-198;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 60
      |||
Db     109 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 168
```

| | | | |
|----|-----|--|-----|
| Qy | 61 | KLYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 120 |
| | | | |
| Db | 169 | KLYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 228 |
| Qy | 121 | IEDFGLHFVRESIKNRCYGGLWEKDQLSIAKKHDPLLREFQEGRLFPPTYKFDRNSNDY | 180 |
| | | | |
| Db | 229 | IEDFGLHFVRESIKNRCYGGLWEKDQLSIAKKHDPLLREFQEGRLFPPTYKFDRNSNDY | 288 |
| Qy | 181 | DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 240 |
| | | | |
| Db | 289 | DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 348 |
| Qy | 241 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY | 300 |
| | | | |
| Db | 349 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY | 408 |
| Qy | 301 | VSIAWVGDSKVSCSDNLNQYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL | 360 |
| | | | |
| Db | 409 | VSIAWVGDSKVSCSDNLNQYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL | 468 |
| Qy | 361 | REDPLGEAQPQI | 372 |
| | | | |
| Db | 469 | REDPLGEAQPQI | 480 |

RESULT 15

PCT-US02-17526-11

; Sequence 11, Application PC/TUS0217526

; GENERAL INFORMATION:

; APPLICANT: EXELIXIS, INC.

; TITLE OF INVENTION: PIBs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

; FILE REFERENCE: EX02-074C-PC

; CURRENT APPLICATION NUMBER: PCT/US02/17526

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US 60/296,076

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/328,605

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/357,253

; PRIOR FILING DATE: 2002-02-15

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 11

; LENGTH: 478

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (56)..(56)

; OTHER INFORMATION: "X" is any amino acid

PCT-US02-17526-11

Query Match 99.6%; Score 2012; DB 1; Length 478;

Best Local Similarity 99.7%; Pred. No. 6.5e-197;

Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|---|--|----|
| Qy | 1 | MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGGGVNICL | 60 |
|----|---|--|----|

| | | | |
|----|-----|---|-----|
| Db | 107 | MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGGGVNICL | 166 |
| Qy | 61 | KLYGYVYSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 120 |
| Db | 167 | KLYGYVYSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 226 |
| Qy | 121 | IEDFGLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLFPPTYKFDRNSNDY | 180 |
| Db | 227 | IEDFGLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLFPPTYKFDRNSNDY | 286 |
| Qy | 181 | DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 240 |
| Db | 287 | DTSEKKRKPAWTDRIWLRLKRQACAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 346 |
| Qy | 241 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY | 300 |
| Db | 347 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY | 406 |
| Qy | 301 | VSIAWVGDSKVSCLDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL | 360 |
| Db | 407 | VSIAWVGDSKVSCLDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL | 466 |
| Qy | 361 | REDPLGEAQPQI | 372 |
| Db | 467 | REDPLGEAQPQI | 478 |

Search completed: February 10, 2005, 18:01:44
Job time : 477 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 17:47:17 ; Search time 23 Seconds
(without alignments)
592.366 Million cell updates/sec

Title: US-09-892-287-1
Perfect score: 2020
Sequence: 1 MDVLSPLSFIKVSHVRMQGI.....FQIPPGSLREDPLGEAQPQI 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 144007 seqs, 36624764 residues

Total number of hits satisfying chosen parameters: 144007

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
 7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
 8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | % Query | | DB | ID | Description |
|---------------|------------|--------------|------|----|---------------------|
| | Score | Match Length | | | |
| 1 | 328 | 16.2 | 908 | 1 | PCT-US04-42360-1594 |
| 2 | 104.5 | 5.2 | 458 | 6 | US-10-450-763-57306 |
| 3 | 90.5 | 4.5 | 497 | 6 | US-10-450-763-33366 |
| 4 | 89.5 | 4.4 | 873 | 6 | US-10-496-011-6 |
| 5 | 89 | 4.4 | 1048 | 6 | US-10-450-763-52226 |
| 6 | 88 | 4.4 | 551 | 6 | US-10-450-763-50598 |
| 7 | 86.5 | 4.3 | 815 | 6 | US-10-496-011-67 |
| 8 | 86.5 | 4.3 | 851 | 6 | US-10-496-011-3 |
| 9 | 85 | 4.2 | 321 | 8 | US-60-643-717-11816 |
| 10 | 85 | 4.2 | 512 | 6 | US-10-450-763-34667 |
| 11 | 85 | 4.2 | 735 | 7 | US-11-021-951-123 |
| 12 | 85 | 4.2 | 1388 | 6 | US-10-450-763-51703 |
| 13 | 84.5 | 4.2 | 716 | 6 | US-10-450-763-43858 |
| 14 | 84.5 | 4.2 | 731 | 6 | US-10-450-763-48706 |
| 15 | 84 | 4.2 | 380 | 1 | PCT-US04-17965-2224 |
| 16 | 83 | 4.1 | 565 | 6 | US-10-450-763-39254 |
| 17 | 83 | 4.1 | 738 | 6 | US-10-450-763-48671 |
| 18 | 83 | 4.1 | 746 | 6 | US-10-450-763-41065 |
| 19 | 83 | 4.1 | 746 | 6 | US-10-450-763-52958 |
| 20 | 83 | 4.1 | 851 | 6 | US-10-450-763-56207 |
| 21 | 83 | 4.1 | 1404 | 6 | US-10-450-763-34552 |
| 22 | 82.5 | 4.1 | 515 | 6 | US-10-450-763-31949 |
| 23 | 82.5 | 4.1 | 1114 | 1 | PCT-US04-42360-604 |
| 24 | 82 | 4.1 | 376 | 6 | US-10-450-763-39711 |
| 25 | 82 | 4.1 | 940 | 6 | US-10-450-763-32557 |
| 26 | 81.5 | 4.0 | 243 | 7 | US-11-031-175-15153 |
| 27 | 81 | 4.0 | 500 | 6 | US-10-450-763-58159 |
| 28 | 81 | 4.0 | 501 | 6 | US-10-450-763-59146 |
| 29 | 81 | 4.0 | 2114 | 6 | US-10-450-763-39435 |
| 30 | 81 | 4.0 | 2356 | 6 | US-10-450-763-39431 |
| 31 | 80.5 | 4.0 | 535 | 8 | US-60-643-717-1969 |
| 32 | 80.5 | 4.0 | 625 | 7 | US-11-031-175-12183 |
| 33 | 80.5 | 4.0 | 631 | 6 | US-10-450-763-52920 |
| 34 | 80.5 | 4.0 | 796 | 7 | US-11-033-545-386 |
| 35 | 80 | 4.0 | 633 | 6 | US-10-450-763-57583 |
| 36 | 80 | 4.0 | 1065 | 6 | US-10-450-763-56125 |

| | | | | | | |
|----|------|-----|------|---|---------------------|-------------------|
| 37 | 80 | 4.0 | 1065 | 6 | US-10-450-763-58750 | Sequence 58750, A |
| 38 | 79.5 | 3.9 | 264 | 7 | US-11-027-399-3617 | Sequence 3617, Ap |
| 39 | 79.5 | 3.9 | 264 | 7 | US-11-027-843-3617 | Sequence 3617, Ap |
| 40 | 79.5 | 3.9 | 264 | 7 | US-11-027-878-3617 | Sequence 3617, Ap |
| 41 | 79.5 | 3.9 | 264 | 7 | US-11-028-169-3617 | Sequence 3617, Ap |
| 42 | 79.5 | 3.9 | 264 | 7 | US-11-028-204-3617 | Sequence 3617, Ap |
| 43 | 79.5 | 3.9 | 264 | 7 | US-11-027-877-3617 | Sequence 3617, Ap |
| 44 | 79.5 | 3.9 | 264 | 7 | US-11-027-879-3617 | Sequence 3617, Ap |
| 45 | 79.5 | 3.9 | 264 | 7 | US-11-028-149-3617 | Sequence 3617, Ap |

ALIGNMENTS

RESULT 1

PCT-US04-42360-1594

; Sequence 1594, Application PC/TUS0442360

; GENERAL INFORMATION:

; APPLICANT: The General Hospital Corporation doing business as Massachusetts General

; APPLICANT: Hospital / Bayer AG

; TITLE OF INVENTION: Nucleotide sequences involved in pain

; FILE REFERENCE: 17633/2048

; CURRENT APPLICATION NUMBER: PCT/US04/42360

; CURRENT FILING DATE: 2004-12-17

; PRIOR APPLICATION NUMBER: 60/531,341

; PRIOR FILING DATE: 19-Dec-2003

; NUMBER OF SEQ ID NOS: 2587

; SOFTWARE: Perl script

; SEQ ID NO 1594

; LENGTH: 908

; TYPE: PRT

; ORGANISM: Rattus norvegicus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: Refseq / NP_445928

; DATABASE ENTRY DATE: 2003-10-05

PCT-US04-42360-1594

Query Match 16.2%; Score 328; DB 1; Length 908;

Best Local Similarity 33.6%; Pred. No. 1.5e-21;

Matches 84; Conservative 44; Mismatches 106; Indels 16; Gaps 6;

| | | | |
|----|-----|---|-----|
| Qy | 9 | FIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICLKLYGYVVS | 68 |
| | | :: :: :: : : : : :: : : : : : | |
| Db | 225 | YVLLASEQLVGVCLFVFIROPQHAPFIRDVAVDTVKTGMGGATGNKGAVAIRMLFHTTSLC | 284 |
| Qy | 69 | IINCHLPPHISNNYQRLEHFDRIL-EMQNCEGRDIFNILDHDLIIWFGDMNFRIEDFGLH | 127 |
| | | : : : : : : : : | |
| Db | 285 | FVCSHFAGQSQVKERNEDFVEIARKLSFPMGR---MLFSHDYVFWCGDFNYRI-DLPNE | 340 |
| Qy | 128 | FVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDYDTSEKKR | 187 |
| | | : : : : : : : : | |
| Db | 341 | EVKELIRQQNWDSLIAQGQLINQKNAGQIFRGFLEGKVTFAPTYKYDLFSEDYDTSEKCR | 400 |
| Qy | 188 | KPAWTDRIWLRLKRQPC--AGPDTPIPPASHFSLSLRGYS----SHMTYG-----ISDHK | 236 |
| | | : : : : : : : : : | |
| Db | 401 | TPAWTDRVLWRRRKWPFDRSAEDLDLLNASFQDESKILYTWTPGTLHYGRAELKTSDDR | 460 |

Qy 237 PVSGTFDLEL 246
|| |:::
Db 461 PVVALIDIDI 470

RESULT 2

US-10-450-763-57306

; Sequence 57306, Application US/10450763

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 790CIP3/US

; CURRENT APPLICATION NUMBER: US/10/450,763

; CURRENT FILING DATE: 2003-06-11

; PRIOR APPLICATION NUMBER: PCT/US01/08631

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 57306

; LENGTH: 458

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (235)..(278)

; OTHER INFORMATION: 1 kw MIND INHIBITOR DIVISION CONTROL domain identified by

; OTHER INFORMATION: eMATRIX, accession number DM01756B, p-value=4.822e-15,

raw score of

; OTHER INFORMATION: 22.91

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (200)..(305)

; OTHER INFORMATION: ParA family ATPase domain identified by PFam, accession
name

; OTHER INFORMATION: ParA, E-value=4.9e-24, PFam score of 93.3

US-10-450-763-57306

Query Match 5.2%; Score 104.5; DB 6; Length 458;

Best Local Similarity 20.9%; Pred. No. 0.12;

Matches 71; Conservative 51; Mismatches 133; Indels 85; Gaps 17;

Qy 46 LFGYWGNGKGGVNICLKLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNI 105
: | : ||| | : :: || : : : | : || |
Db 108 VIGVAAHKGGV-----YKTSVSVHLAQDLAL-----KGLRVLLVEGNDPQGT 149

Qy 106 --LDHDLIIWFGDMNFRIEDFGLHF-----VRESIKNRCYGGL-WEKDQLSIAKKHDP 155
: | | | : | | | : || | : || | : :
Db 150 ASMYHG---WVPDLHIHAEDTLLPFYLGEKDDVTYAIKPTCWPGLDIIPSCALHRIETE 206

Qy 156 LLREFQEGRLLFPP----TYKFDRNSNDYDTSEKKRKP---AWTDRILWRLKRQPCAGPD 208
| : : | || : | : : || | | : : ||
Db 207 LMGKFDEGKLPTDPLMLRLAIETVAHDYDVIVIDSAPNLGIGTINVV-----CAADV 259

```

Qy      209 TPIP-PASHFSLSLRGYSSHMTYGISDHKPVSGTFDLELKPLVSAPLIVLMPEDLWTVEN 267
      :| || | :| : : ||: | : | :| : :
Db      260 LIVPTPAELFD-----YTSALQF-----FDMLRDLLKNVDLKGFEPAKKWLAGH 303

Qy      268 DMMVSYSSSTDFPSSPWDWIGL-YKVGLRDVNDYVSYAWV---GDSKVSCSDNLNQVYI 322
      : : |:: | : | :| : | | :| | : || : | : | : :
Db      304 EQYIFYAN-SELPKNPRGGLGVRYPGGPHNVPDNLD--WVHLLYNGGQAPCMKSNNALIV 360

Qy      323 DISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSLRE 362
      : : ||| : || ||:
Db      361 ILGTVTL-----DAVGIGLVMPVLPGLLRD 385

```

RESULT 3

US-10-450-763-33366

; Sequence 33366, Application US/10450763

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 790CIP3/US

; CURRENT APPLICATION NUMBER: US/10/450,763

; CURRENT FILING DATE: 2003-06-11

; PRIOR APPLICATION NUMBER: PCT/US01/08631

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 33366

; LENGTH: 497

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (235)..(278)

; OTHER INFORMATION: 1 kw MIND INHIBITOR DIVISION CONTROL domain identified by

; OTHER INFORMATION: eMATRIX, accession number DM01756B, p-value=4.822e-15,

raw score of

; OTHER INFORMATION: 22.91

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (200)..(307)

; OTHER INFORMATION: Para family ATPase domain identified by PFam, accession name

; OTHER INFORMATION: Para, E-value=6.5e-23, PFam score of 89.5

US-10-450-763-33366

Query Match 4.5%; Score 90.5; DB 6; Length 497;

Best Local Similarity 20.5%; Pred. No. 2.4;

Matches 84; Conservative 59; Mismatches 138; Indels 129; Gaps 23;

```

Qy      46 LFGYWGNKGGVNICLKLYGYYSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNI 105
      : | : ||| | : : : || : : : | : || |
Db      108 VIGVAAHKGGV-----YKTSVSVHQAQDLAL-----KGLRVLLVEGNDPQGT 149

```

Qy 106 --LDHDLIIWFGDMNFRIEDFGLHF-----VRESIKNRCYGGL-WEKDQLSIKKHDP 155
 : | | | : | | | : | | | : :
 Db 150 ASMYHG---WVPDLHIHAEDTLLPFYLGEKDDVTYAIKPTCWPGLDIIPSCALHRIETE 206
 Qy 156 LLREFQEGRLLFPP---TYKFDRNSNDYDTSEKKRKP---AWTDRILWRLKRQPCAGPD 208
 | : | | : | : : | | | : : | |
 Db 207 LMGKFDEGKLPTDPHMLRLAIETVAHDYDVIVIDSAPNLGIGTINVV-----CAADV 259
 Qy 209 TPIP-PASHF-----SLSLRGYSSHMTYGISDHKPVSGTFDLELKPLV 250
 : | | | : : | : : : : | : | |
 Db 260 LIVPTPAELFDYTSALQFFDMLRDLLKNVDLKGFEPTSVSTVTLPSLTLNL-LPPSY 318
 Qy 251 SAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSP----- 283
 | : | | : : : : | | : |
 Db 319 KDPCDYIGP--TWTIQDNLPISRSLT--LTTSPKFFLPSERLSSSWLDVRHIEKYVDQGK 374
 Qy 284 -----WDW-----IG-----LYKVGLRD-----VNDYVSYAWVGDSKVS CSDNLNQV- 320
 | | | | : | : : | | : : : |
 Db 375 SGTRELLWSWAQKNKTIGDLLQVLQEMGHRAIHLITNYVRHA-VTKSATATATGYQEV 433
 Qy 321 ----YIDISNIPTTEDEFLLCYSNSLSRVVGISRPFQIPPGSLRED-PL 365
 : : : | : | : | | | : | : : |
 Db 434 NSEQILDLTKAP---EVFAIPIQGNRLRGVVLVVGFRGV--SQLKEEHPL 478

RESULT 4

US-10-496-011-6

; Sequence 6, Application US/10496011
 ; GENERAL INFORMATION:
 ; APPLICANT: BOURGERON, THOMAS
 ; APPLICANT: JAMAIN, STEPHANE
 ; APPLICANT: QUACH, HELENE
 ; APPLICANT: BETANCUR, CATALINA
 ; APPLICANT: LEBOYER, MARION
 ; APPLICANT: GILLBERG, CHRISTOPHER
 ; TITLE OF INVENTION: POLYNUCLEOTIDE AND PROTEIN INVOLVED IN SYNAPTOGENESIS,
 VARIANTS
 ; TITLE OF INVENTION: THEREOF, AND THEIR THERAPEUTIC AND DIAGNOSTIC USES
 ; FILE REFERENCE: 253820US0XPCT
 ; CURRENT APPLICATION NUMBER: US/10/496,011
 ; CURRENT FILING DATE: 2004-05-28
 ; PRIOR APPLICATION NUMBER: PCT/FR02/04134
 ; PRIOR FILING DATE: 2002-11-28
 ; PRIOR APPLICATION NUMBER: CA2364106
 ; PRIOR FILING DATE: 2001-11-30
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 6
 ; LENGTH: 873
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-496-011-6

Query Match 4.4%; Score 89.5; DB 6; Length 873;
 Best Local Similarity 18.8%; Pred. No. 6.4;
 Matches 85; Conservative 59; Mismatches 134; Indels 173; Gaps 22;

| | | | |
|----|-----|--|-----|
| Qy | 5 | SPLSFQIKVSH-----VRMQGILLLVFA-KYQHLPIYIQLSTKSTPTGLFGYWGNGK | 54 |
| | | : : : : : : : | |
| Db | 315 | SCVSLTLTSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILA-----DKV | 361 |
| Qy | 55 | GVNI-----CLKLYGYVVSIIINCHLP-----PHISNNYQRLEH | 87 |
| | | : : | |
| Db | 362 | GCNMLDTTDMVECLKNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLN | 421 |
| Qy | 88 | FDRILEMQNCEG-RDIPNILDHDLIIWFGDMNFRIEDF-----GLHFVRESIKNRC | 137 |
| | | : : : : : : : : : : : : | |
| Db | 422 | YDIMLGVNQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIK-FM | 480 |
| Qy | 138 | YGGLWEKDQLSIAKKHDPLLREFQEGRLLP-----PTYKFDRNSNDYDTSE | 184 |
| | | : : : : : : : : : | |
| Db | 481 | YTDWADKENPETRRK--TLVALFTDHQWVAPAVATADLHAQYGSPTYFY----AFYHHCQ | 534 |
| Qy | 185 | KKRKPAWTDRILWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSGTFDL | 244 |
| | | : : : | |
| Db | 535 | SEMKPSWAD-----SAHGDEVYPYVFGI----- | 556 |
| Qy | 245 | ELKPLVSAPLIVLMPEDLWTV---ENDMMVS-----YSSTSDFPSSPWDWIGLYKV | 292 |
| | | : : : : : : : : : | |
| Db | 557 | ---PMIG-----PTELFSCNFSKNDVMLSAVVMTYWTNFAKTGD-PNQVP----- | 598 |
| Qy | 293 | GLRDV-----NDYVSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEF-----L | 335 |
| | | : : : : : | |
| Db | 599 | --QDTKFIHTKPNRFEEVAW---SKYNPKD---QLYLHIGLKPRVRDHYRATKVAFWLEL | 650 |
| Qy | 336 | LCYYSNSLRSVVGISRPFQIPPGSLREDPLG | 366 |
| | | : : : : : | |
| Db | 651 | VPHLHNLNEIFOYVSTTTTKVPPPDMTSFYGY | 681 |

```

US-10-450-763-52226
; Sequence 52226, Application US/10450763
; GENERAL INFORMATION:
;   APPLICANT: Hyseq, Inc
;   TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;   FILE REFERENCE: 790CIP3/US
;   CURRENT APPLICATION NUMBER: US/10/450,763
;   CURRENT FILING DATE: 2003-06-11
;   PRIOR APPLICATION NUMBER: PCT/US01/08631
;   PRIOR FILING DATE: 2001-03-30
;   PRIOR APPLICATION NUMBER: 09/540,217
;   PRIOR FILING DATE: 2000-03-31
;   PRIOR APPLICATION NUMBER: 09/649,167
;   PRIOR FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 60736
;   SOFTWARE: Custom
; SEQ ID NO 52226
;   LENGTH: 1048
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: DOMAIN

```

```
; TYPE: PRT
```

ORGANISM: Homo sapiens

; FEATURE:

```
; NAME/KEY: DOMAIN
```

```
; LOCATION: (410)..(439)
; OTHER INFORMATION: kw REPLICATION REPB REPA INITIATION domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM00653A, p-value=7.207e-27,
raw score of
; OTHER INFORMATION: 20.40
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (651)..(765)
; OTHER INFORMATION: ParA family ATPase domain identified by Pfam, accession
name
; OTHER INFORMATION: ParA, E-value=2.7e-28, Pfam score of 107.5
US-10-450-763-52226
```

```
Query Match          4.4%; Score 89; DB 6; Length 1048;
Best Local Similarity 21.4%; Pred. No. 9;
Matches 75; Conservative 47; Mismatches 112; Indels 116; Gaps 19;
```

```
Qy      46 LFGYWGNGKGGVNICLKLYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNI 105
      : | : ||| | : : : | : : | | |
Db      558 VIGVAAHKGGV-----YKTSVSVHLAQDLAL-----KGLRVLLVEGNDPQGT 599

Qy      106 --LDHDLIIWFGDMNFRIEDFGLHF-----VRESIKNRCYGGL-WEKDQLSIAKKHDP 155
      : | | | : | : | | | : || | : | | | : : :
Db      600 ASMYHG---WVPDLHIHAEDTLLPFYLGEKDDVTYAIKPTCWPGLDIIPSCALHRIETE 656

Qy      156 LLREFQEGRLLFPP-----TYKFDRNSNDYDTSEKKRKP---AWTDRILWRLKRQPCAGPD 208
      | : | || : | : : ||| | : || | : : | |
Db      657 LMGKFDEGKLPTDPHMLRLAIETVAHDYDVIVIDSAPNLGIGTINVV-----CAADV 709

Qy      209 TPIP-PASHFSLSLRGYSSHMTYGISDHKPVSGTFDLELKPLVSAPLIVLMPEDLWTVEN 267
      : | || | : | : : : || : | : | : | | |
Db      710 LIVPTPAELFD-----YTSALQF-----FDM-LRDL-----LKNVDLKGFEF 745

Qy      268 D--MMVSYSSSTSDFPSSPW-----DWIGLYKVG----- 293
      | : : : | | : || | : | |
Db      746 DVRILLTKYSNSNGSQSPWMEEQIRDAWGSMLKNVVRETDEVG--KVAEYNGYHFVFAL 803

Qy      294 -----LRDVNDYVSYAWVGDSKVS CSDN LNQVYID----ISNIPTTEDE 333
      | : | : | ||| : : | : | : : | : |
Db      804 AGSPKDAVDTSIYMFYQKVG DNSIDSWKNAGRVFKDSDKFVANDPILKDQ 853
```

RESULT 6

```
US-10-450-763-50598
; Sequence 50598, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
```



```
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 50598
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(551)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-50598
```

```
Query Match          4.4%; Score 88; DB 6; Length 551;
Best Local Similarity 22.8%; Pred. No. 4.7;
Matches 64; Conservative 39; Mismatches 84; Indels 94; Gaps 19;
```

```
Qy      4 LSPLSFIKVSHVRMQGIL---LLVFAKY-----QHL-----PYIQILSTKSTPTGLFG 48
      ||| ::  | | ||:  | ||:|:  ||:  ||:  |
Db      188 LSP-TYPAHHFR-SGIIGSGLCVFSKHPIQELTQHIYTLNGYPYMI-----HHG 235

Qy      49 YWGNKGGVN-ICLKLYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILD 107
      | :  | : | | | ::  ||  |  | :  |  |  :  ::  :
Db      236 DWFGSKAVGLLVHLHNGMELNAYVTHL--HAEYNRQK----DIYLTSLVGVQAWELAQFIH 289

Qy      108 H-----DLIIWFGDMNFRIEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPDLL--REF 160
      |  |::: ||:|  ||  |  ::|  : ||  |  |  | :|
Db      290 HTSKKADVLLCGDLNMHPEDLGCCLLKE-----WTGL-----HDAYLETRDF 332

Qy      161 ---QEGRLLPPTYKFDNRNSNDYDTSEKKRKP---AWTDRILWRLKRQPCAGPDTPIPP 213
      :|| : |  | |  |::: ||  |  :||:
Db      333 KGSEEGNTMVP-----KNCY-VSQQELKPFPGVVRIDYVLYK-----A 369

Qy      214 ASHFSLSLR-----GYSSHMTYGISDHKPVSGTFDLELKP 248
      | | : | :  | :  |  :|||: :  | :  |
Db      370 VSGFYISCKSFETTTGFDPHSGTPLSDHEALMATLFVRHSP 410
```

RESULT 7

US-10-496-011-67

; Sequence 67, Application US/10496011

; GENERAL INFORMATION:

; APPLICANT: BOURGERON, THOMAS

; APPLICANT: JAMAIN, STEPHANE

; APPLICANT: QUACH, HELENE

; APPLICANT: BETANCUR, CATALINA

; APPLICANT: LEBOYER, MARION

; APPLICANT: GILLBERG, CHRISTOPHER

; TITLE OF INVENTION: POLYNUCLEOTIDE AND PROTEIN INVOLVED IN SYNAPTOGENESIS, VARIANTS

; TITLE OF INVENTION: THEREOF, AND THEIR THERAPEUTIC AND DIAGNOSTIC USES

; FILE REFERENCE: 253820US0XPCT

; CURRENT APPLICATION NUMBER: US/10/496,011

; CURRENT FILING DATE: 2004-05-28

; PRIOR APPLICATION NUMBER: PCT/FR02/04134

; PRIOR FILING DATE: 2002-11-28

; PRIOR APPLICATION NUMBER: CA2364106

; PRIOR FILING DATE: 2001-11-30

```
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67
; LENGTH: 815
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-496-011-67
```

```
Query Match          4.3%; Score 86.5; DB 6; Length 815;
Best Local Similarity 18.6%; Pred. No. 11;
Matches    84; Conservative    60; Mismatches   134; Indels   173; Gaps    22;
```

```
Qy      5 SPLSFIKVSH-----VRMQGILLLVFA-KYQHLPYIQILSTKSTPTGLFGYWGNGK 54
      | :| : :||          : | | :| || | :||:          :|
Db      257 SCVSLTLTSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILA-----DKV 303

Qy      55 GVNI-----CLKLYGYVSIINCHLP-----PHISNNYQRLEH 87
      | |:          ||: | | |          | |          :
Db      304 GCNMLDTTDMVECLRNKNYKELIQQTTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLN 363

Qy      88 FDRILEMQNCEG-RDIPNILDHDLIIWFGDMNFRIEDF-----GLH FVRESIKNRC 137
      :| :| : || : : |:|: : | :| : :|          | :||:|
Db      364 YDIMLGVNQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIK-FM 422

Qy      138 YGGLWEKDQLSIAKKHDPLLREFQEGRLLP-----PTYKFDRNSNDYDTSE 184
      | :|:          :| | : | : : |          ||| : | :
Db      423 YTDWADKENPETRRK--TLVALFTDHQWVAPAVATADLHAQYGSPTYFY----AFYHHCQ 476

Qy      185 KKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSGTFDL 244
      : ||:| |          | |          :||
Db      477 SEMKPSWAD-----SAHGDEVPPYVFGI----- 498

Qy      245 ELKPLVSAPLIVLMPEDLWTV---ENDMMVS-----YSSTSDFPSSPWDWIGLYKV 292
      |::          | :|:: :||:|:|          :: | | |:|
Db      499 ---PMIG-----PTELFSCNFSKNDVMLS AVVMTYWTNFAKTGD-PNQVP----- 540

Qy      293 GLRDV-----NDYVSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEF-----L 335
      :|          | : || || : | |:|: | | | :          |
Db      541 --QDTKFIHTKPNRFEEVAW---SKYNPKD---QLYLHIGLKPRVRDHYRATKVAFWLEL 592

Qy      336 LCYYSNSLRSVVGISRPFQIPPGSLREDPLG 366
      : : |          :| ::|| : | |
Db      593 VPHLHNLNEIFQYVSTTTTKVPPDMTSFPYG 623
```

RESULT 8

US-10-496-011-3

; Sequence 3, Application US/10496011

; GENERAL INFORMATION:

; APPLICANT: BOURGERON, THOMAS

; APPLICANT: JAMAIN, STEPHANE

; APPLICANT: QUACH, HELENE

; APPLICANT: BETANCUR, CATALINA

; APPLICANT: LEBOYER, MARION

; APPLICANT: GILLBERG, CHRISTOPHER

; TITLE OF INVENTION: POLYNUCLEOTIDE AND PROTEIN INVOLVED IN SYNAPTOGENESIS, VARIANTS

```
; TITLE OF INVENTION:  THEREOF, AND THEIR THERAPEUTIC AND DIAGNOSTIC USES
; FILE REFERENCE: 253820US0XPCT
; CURRENT APPLICATION NUMBER: US/10/496,011
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: PCT/FR02/04134
; PRIOR FILING DATE: 2002-11-28
; PRIOR APPLICATION NUMBER: CA2364106
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
;   LENGTH: 851
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-496-011-3
```

```
Query Match          4.3%; Score 86.5; DB 6; Length 851;
Best Local Similarity 18.6%; Pred. No. 11;
Matches 84; Conservative 60; Mismatches 134; Indels 173; Gaps 22;
```

```
Qy      5 SPLSFIKVSH-----VRMQGILLLVFA-KYQHLPYIQILSTKSTPTGLFGYWGNGK 54
      | : | : : | | : | | : | | : | | : | : | : | : |
Db      293 SCVSLTLTSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILA-----DKV 339

Qy      55 GVNI-----CLKLYGYVSIINCHLP-----PHISNNYQRLEH 87
      | | : | | : | | : | | : | | : | | : | : | : |
Db      340 GCNMLDTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLN 399

Qy      88 FDRILEMQNCEG-RDIPNILDHDLIIWFGDMNFRIEDF-----GLHFVRESIKNRC 137
      : | : | : | : | : | : | : | : | : | : | : | : |
Db      400 YDIMLGVNQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIK-FM 458

Qy      138 YGGLWEKDQLSIAKKHDPLLRREFQEGRLLFP-----PTYKFDRNSNDYDTSE 184
      | : | : | : | : | : | : | : | : | : | : | : |
Db      459 YTDWADKENPETRRK--TLVALFTDHQWVAPAVATADLHAQYGSPTYFY----AFYHHCQ 512

Qy      185 KKRKPAWTDRILWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSGTFDL 244
      : | | : | | : | | : | | : | | : | | : | |
Db      513 SEMKPSWAD-----SAHGDEVVPYVFGI----- 534

Qy      245 ELKPLVSAPLIVLMPEDLWTV---ENDMMVS-----YSSTSDFPSSPWDWIGLYKV 292
      | : : | : | : | : | : | : | : | : | : | : |
Db      535 ---PMIG-----PTELFSCNFSKNDVMLS AVVM TYWTNFAKTGD-PNQPV P----- 576

Qy      293 GLRDV-----NDYVSYAWVGDSKVS CSDN LNQVYIDISNIPTTEDEF-----L 335
      : | : | : | : | : | : | : | : | : | : | : |
Db      577 --QDTKFIHTKPNRFEEVAW---SKYNPKD---QLYLHIGLKPRVRDHYRATKVAFWLEL 628

Qy      336 LCYYSNSLRSVVGISR.PFQIPPGSLREDPLG 366
      : : | : | : : | : | : | : | : | : |
Db      629 VPHLHNLNEIFQYVSTTTKVPPPDMTSFPYG 659
```

```
RESULT 9
US-60-643-717-11816
; Sequence 11816, Application US/60643717
; GENERAL INFORMATION:
```

```
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)A
; CURRENT APPLICATION NUMBER: US/60/643,717
; CURRENT FILING DATE: 2005-01-12
; NUMBER OF SEQ ID NOS: 19247
; SEQ ID NO 11816
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Candidatus Blochmannia floridanus
US-60-643-717-11816
```

```
Query Match          4.2%; Score 85; DB 8; Length 321;
Best Local Similarity 23.8%; Pred. No. 4.3;
Matches 35; Conservative 23; Mismatches 67; Indels 22; Gaps 5;
```

```
Qy      51 GNKGGVN----ICLKLYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNIL 106
      |:| || :| | ||: : :| | | : : | :|:| || |
Db      177 GHKAAVNHVNLCKKAGAKYVTTLPISVPSHCSIMKKMVSRLFQKIIENTVISSPKIPVIN 236

Qy      107 DHDLIIWFGDMNFRIEDFGLHFVRESIKNRCYGGGL-WEKDQLSIAKKHDPLLREFQEG-- 163
      : |: | : | |:|:|: : | : | : | : : | | |
Db      237 NVDVSI-----EQEPQFIRDSLIRQLYNPVRWNEIMQEFINKDIKIVLEMGPVKV 286

Qy      164 --RLFPPTYK---FDRNSNDYDTSEK 185
      ||: | | : || |: |
Db      287 LTRLIQRSVYSDSLFSLINDVDSLK 313
```

RESULT 10

US-10-450-763-34667

```
; Sequence 34667, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CUPRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 34667
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (116)..(143)
; OTHER INFORMATION: Mrp family proteins domain identified by eMATRIX,
accession
; OTHER INFORMATION: number BL01215A, p-value=4.964e-11, raw score of 9.75
; FEATURE:
```

```
; NAME/KEY: DOMAIN
; LOCATION: (211)..(302)
; OTHER INFORMATION: ParA family ATPase domain identified by PFam, accession
name
; OTHER INFORMATION: ParA, E-value=0.011, PFam score of -1.9
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(512)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-34667
```

```
Query Match          4.2%; Score 85; DB 6; Length 512;
Best Local Similarity 21.6%; Pred. No. 8;
Matches   68; Conservative   43; Mismatches 124; Indels   80; Gaps   16;
```

```
Qy      46 LFGYWGNGKGGVNICLKLYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCCEGRDIPNI 105
      : | : ||| | : :: || :: : | : || |
Db      119 VIGVAAHKGGV-----YKTSVSVHLAQDLAL-----KGLRVLLVEGNDPQGT 160

Qy      106 --LDHDLIIWFGDMNFRIEDFGLHF-----VRESIKNRCYGGGL-WEKDQLSIKKHDP 155
      : | | | : | | | | : || | : || | : :
Db      161 ASMYHG---WVPDLHIHAEDTLLPFYLGEKDDVTYAIKPTCWPGLDIIPSCALHRIETE 217

Qy      156 LLREFQEGRLLFPP---TYKFDRNSNDYDTSEKKRKP---AWTDRILWRLKRQPCAGPD 208
      | : : | || : | : : || | | : | ||
Db      218 LMGKFDEGKLPTDPHMLRLGIETVAHDYDVLVIDSPPNLGIGTINVRWAADVQP----- 272

Qy      209 TPIPPASHFSLSLRGYSSHMTYGISDHKPVSGTFDLE-LKPLVSAPLIVLMPEDLWTVEN 267
      | : : | : || : | : || : : | | : : |
Db      273 -----LXIPKQQQNEKYQVPQ-----FDQSTIKNIESAKGLDVW--DSWPLQN 313

Qy      268 -DMMVS----YSSTSDFPSSPWDWIGLYKVGLRDVNDYVSYAWVGDSKVSCSDNLNQVYI 322
      | | : | || | | : | : | || : : | : :
Db      314 ADGTVAEYNGYHVVFALAGSPKD-----ADDTSIYMFYQKVGDNSIDSWKNAGRVFK 365

Qy      323 DI----SNIPTTEDE 333
      | : | : | :
Db      366 DSDKFDANDPILKDQ 380
```

RESULT 11

```
US-11-021-951-123
; Sequence 123, Application US/11021951
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMEIER, Christian
; APPLICANT: Kettling, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.0002U5
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
```

; PRIOR APPLICATION NUMBER: 60/543,518
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/524,960
 ; PRIOR FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: EP 04003058
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: EP 03025871
 ; PRIOR FILING DATE: 2003-11-11
 ; PRIOR APPLICATION NUMBER: EP 03025851
 ; PRIOR FILING DATE: 2003-11-10
 ; PRIOR APPLICATION NUMBER: EP 03013819
 ; PRIOR FILING DATE: 2003-06-18
 ; NUMBER OF SEQ ID NOS: 191
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 123
 ; LENGTH: 735
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-021-951-123

Query Match 4.2%; Score 85; DB 7; Length 735;
 Best Local Similarity 18.9%; Pred. No. 13;
 Matches 68; Conservative 53; Mismatches 136; Indels 102; Gaps 14;

Qy 62 LYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDH-DLIIWFGDMNFR 120
 | ||| | :| | ::: | : : | :|| : | | : :
 Db 19 LLGYFSDLNFCAPMVVTSS-----TTGDLSSIPSELENIPSENQYFQSAIWSGFIKVK 72

Qy 121 IEDFGLHFVRESIKNRCYGGWLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDNRNSND- 179
 | : | | : :| || | | : :|| | : :| :
 Db 73 KSD--EYTFATSADN--HVTMWVDDQEVINKASNSNKIRLEKGR-LYQIKIQYQRENPT 127

Qy 180 -----YDTSEKKRKPAWTDRIW-----RLKRQPCAGPDTP-----IPPAS 215
 : | : |:: :| : | || ||| | ||
 Db 128 KGLDFKLYWTDSONKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIPD-- 185

Qy 216 HFSLSLRGY-----SSHMTYGI-----SDHKPVSGTF 242
 || : || : | | : || : | :|
 Db 186 --SLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVTGRI 243

Qy 243 DLELKPLVSAPLIVLMP-----EDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRD 296
 | : | ||: | |:: :|: : : :| |
 Db 244 DKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSQ-----TRT 288

Qy 297 VNDYVSYAWVGDSKVSCLNQLNQYIDISNIPTTEDEFLLCYYSNSLSRVVVGISRPFQI 355
 :: | : | :| : : : || : :||| | | :
 Db 289 ISKNTSTSRHTTSEVHGNAEVHASFFDIGGSVSAG-----FSNSNSSTVAIDHSLSL 340

RESULT 12

US-10-450-763-51703
 ; Sequence 51703, Application US/10450763
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 790CIP3/US
 ; CURRENT APPLICATION NUMBER: US/10/450,763

```

; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 51703
; LENGTH: 1388
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1293)..(1318)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases family 2 proteins
; OTHER INFORMATION: domain identified by eMATRIX, accession number BL00972D,
p-value=
; OTHER INFORMATION: 7.750e-19, raw score of 22.55
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1290)..(1350)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family domain
; OTHER INFORMATION: identified by PFam, accession name UCH-2, E-value=1.1e-
26, PFam
; OTHER INFORMATION: score of 102.0
US-10-450-763-51703

```

```

Query Match          4.2%; Score 85; DB 6; Length 1388;
Best Local Similarity 20.5%; Pred. No. 30;
Matches 83; Conservative 59; Mismatches 160; Indels 102; Gaps 22;

```

```

Qy      32 PYIQILSTKSTPTGLFG--YWGN--KGGVNICLKLY-GYYVSIINCHLPPHISNNYQRLE 86
      ||::: : | | : : | : | | : | || :
Db      665 PYVELKDSGRPDWEVAEAWDNHLRRNRSIIVDLFHGLQRSQVKCKTCGHISVRFDPFN 724

Qy      37 HFDRILEMQNCEGRDIPNI-LDHDLIWFG-DMNFRIEDFGLHFVRESIKNRCYGGGLEW 144
      | | : : | | | : : | : | | : : : | |
Db      725 FLSLPLPMDSYMDEITVIKLDGTTVPVRYGLRLNMDEKYTGL---KKQLRDLC--GL-NS 778

Qy      145 DQLSIAKKHDPDLLREFQEGRLFPPTYKFDRNSNDYDTSEKKRKPATDRILWRLKRQPC 204
      :|: :|: || :::| | | : | | : | :
Db      779 EQILLAEVHDSNIKDFSSS----PST----NGMFTLTNGDLPKPIFI-----PN 820

Qy      205 AGPDTPIPPASHFSLSLRGYSSHMT-----YGISDHKPVSGTFDLELKPLVSAPLI 255
      |:| :| : : : : : | | | :|: :| : | | :| :
Db      821 GMPNTVVPCGTEKNFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSPQENRPSL 880

Qy      256 VLMPEDLWTVENDMMVS---YSSTSDFPSSPW---DWIG----- 288
      || : :| : : | : | :
Db      881 FGMP-----LIVPCTVHTQKKDLYDAVWIQVSWLARPLPPQEASIIHAQDRDNCMGY 931

Qy      289 LYKVGLRDV-NDYVSYAWVGD-----SKVSCSDN---LNQVYIDISNIPTTEDEFLLCY 338
      | || | | :| | | :| : : : | | : | |
Db      932 QYPFTLRVVQKDGISCAWCPQYRFCRGCKIDCGEDRAFIGNAYIAVDWHPTA---LHLRY 988

```

Qy 339 YSNSLRSV-----VGISRPFQIPPGSL-----REDPLGEAQ 369
:: | | | | | | : | | | :
Db 989 QTSQERVVDKHESVEQSRRQAEPINLDSCLRAFTSEEELGESE 1032

RESULT 13

US-10-450-763-43858

; Sequence 43858, Application US/10450763

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 790CIP3/US

; CURRENT APPLICATION NUMBER: US/10/450,763

; CURRENT FILING DATE: 2003-06-11

; PRIOR APPLICATION NUMBER: PCT/US01/08631

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 43858

; LENGTH: 716

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (235)..(278)

; OTHER INFORMATION: 1 kw MIND INHIBITOR DIVISION CONTROL domain identified by

; OTHER INFORMATION: eMATRIX, accession number DM01756B, p-value=4.822e-15,

raw score of

; OTHER INFORMATION: 22.91

US-10-450-763-43858

Query Match 4.2%; Score 84.5; DB 6; Length 716;

Best Local Similarity 22.7%; Pred. No. 14;

Matches 61; Conservative 30; Mismatches 89; Indels 89; Gaps 16;

Qy 138 YGGLW---EKDQLSIAKKHDPLLREFQEGRL-LF-----PPTYKF-----DRNSNDYDT 182
| | | | | | : | | | : | :

Db 427 YGESWNLRLADQRLIFAKSWPRASRYQQGHQDLFILRSDLPSQVFIIRDKLMERRNRRTGR 486

Qy 183 SEKKRKPAWTDRI--WRLKRQPCAGPD-----TPIPPASHFSLSLRGYSSHMTY----- 230
: | | | | | : | : | | : | | |

Db 487 TEKARIWEVTDRTVVRTWIGEAVAAAAADGVTFSPVTPHTF----RHSYAMHMLYAGIPL 542

Qy 231 ----GISDHKPVSGT-----FDLELKPLVSAPLIV-----LMPE----- 260
: | | : | | | : | : | : | :

Db 543 KVLQSLMGHKSISSTEYTKVFALD---VAAPARIPKQQQNEKYQVPQFDQSTIKNIES 598

Qy 261 -----DLWTIVEN-DMMVS---YSSTSDFPSSPWDWIGLYKVGLRDVNDYVSYAWVGD 308
| | : | | | : | | | | : | | |

Db 599 AKGLDVWDSWPLQNADGTVAEYNGYHVVFALAGSPKD-----ADDTSIYMFYQKVGD 650

Qy 309 SKVSCSDNLNQVYIDI----SNIPTTEDE 333
: : | : | : | : | :

Db 651 NSIDSWKNAGRVFKDSDKFDANDPILKDQ 679

RESULT 14

US-10-450-763-48706

; Sequence 48706, Application US/10450763

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 790CIP3/US

; CURRENT APPLICATION NUMBER: US/10/450,763

; CURRENT FILING DATE: 2003-06-11

; PRIOR APPLICATION NUMBER: PCT/US01/08631

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 48706

; LENGTH: 731

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (620)..(635)

; OTHER INFORMATION: GLYCOSYL HYDROLASE FAMILY 1 SIGNATURE domain identified by

; OTHER INFORMATION: eMATRIX, accession number PR00131A, p-value=1.563e-11, raw score of

; OTHER INFORMATION: 12.98

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (531)..(719)

; OTHER INFORMATION: Glycosyl hydrolase family 1 domain identified by PFam,

; OTHER INFORMATION: accession name Glyco_hydro_1, E-value=1.3e-43, PFam score of 155.2

US-10-450-763-48706

Query Match 4.2%; Score 84.5; DB 6; Length 731;

Best Local Similarity 18.5%; Pred. No. 14;

Matches 74; Conservative 48; Mismatches 119; Indels 159; Gaps 19;

```
Qy      54 GGVNICLK-LYGYVSIINC-HLP-----PHISNNYQRLEHF 88
      | :| || | :||| :| |:|
Db      343 GNINNALKYAKGEFVSIFDCDHVPTRSFLQMTMGWFLKEKQLAMMQTPH---HFFSPDPF 399

Qy      89 DRILEMQNCEGRDIPNILDHDLIIWFG-----DMNFRIEDFGLHFVRESIKNRCYGGLWE 143
      :| | | | : || : ::| : | | || |:| |
Db      400 ERNLG---RFRKTPN---EGTLFYGLRQSWEFNAR---GLELVKEGRAQACVSAGNT 447

Qy     144 KDQLSIAKKHDP LLR--EFQEGRL LFPPTYKFDRNSNDYDTSEKKRKPAWTDRI LWR LKR 201
      : :|| | | : | | |:|
Db     448 GALMGLAKL---LLKPLEGQNHRMLL-----RWEAKLAALVRL 482

Qy     202 QPCAGPDTP IPPAS-----HFSLSLRGYSSHMTYGISDHKPVSGTFDLELKLPLVSA 252
```

| | | | |
|----|-----|--|-----|
| Db | 483 | QENTAQPVPFAPNNARPLTLEDDRLSCTVRGYNFAITFSKMSGKPTSW-----QLVAS | 535 |
| Qy | 253 | PLIVLM-----PEDLWTV-----ENDMMVSYSSSTSDFPS- | 281 |
| Db | 536 | ALATKIAHEVNPQNQVGCMLAGGNFYYPYSCKPEDVWAALEKDRENLFIDVQARGTYPAY | 595 |
| Qy | 282 | -----SPWDWIGLYKVGLRDVNDYVSYAWVGDSKVSCSDNLNQVYIDISNI | 327 |
| Db | 596 | SARVFREKGVITINKAPGD-----DEILKNTVDFVSFSYYASRCASAEMNANN----- | 642 |
| Qy | 328 | PTTEDEFLLCYYSNLSRVVGISRPF-QIPPGSLREDPLG | 366 |
| Db | 643 | -----SSAANVVKSLRNPYLQVSDWGWGIDPLG | 670 |

RESULT 15

PCT-US04-17965-2224

; Sequence 2224, Application PC/TUS0417965

; GENERAL INFORMATION:

; APPLICANT: ARBORGES, LLC
; APPLICANT: BLOKSBERG, LEONARD N.
; APPLICANT: BRYANT, CATHERINE
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: FROST, MICHAEL J.
; APPLICANT: FORSTER, RICHARD LLEWELLYN SYDNEY
; APPLICANT: GRIGOR, MURRAY
; APPLICANT: HIGGINS, COLLEEN
; APPLICANT: LASHAM, ANNETTE
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: PUTHIGAE, SATHIAH
; APPLICANT: VEERAKONE, STELLA
; APPLICANT: WESTWOOD, CLAIRE
; APPLICANT: GAUSE, KATRINA
; APPLICANT: WOOD, MARION
; APPLICANT: ROTTMAN, WILLIAM
; APPLICANT: HAVUKKALA, ILKKA

; TITLE OF INVENTION: TRANSCRIPTION FACTORS

; FILE REFERENCE: 044463-0296

; CURRENT APPLICATION NUMBER: PCT/US04/17965

; CURRENT FILING DATE: 2004-06-07

; PRIOR APPLICATION NUMBER: 60/476,189

; PRIOR FILING DATE: 2003-06-06

; NUMBER OF SEQ ID NOS: 3679

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 2224

; LENGTH: 380

; TYPE: PRT

; ORGANISM: Pinus radiata

PCT-UC04-17965-2224

Query Match 4.2%; Score 84; DB 1; Length 380;

Best Local Similarity 21.4%; Pred. No. 6.7;

Matches 65; Conservative 37; Mismatches 96; Indels 106; Gaps 16;

Qy 92 LEMQNCEGRDIPNILDHDLIIWFGDMNFRIEDFGLHFVRESIKNR-CYGGL----- 141
 ||:| || |:|: | : : : || | : ||
 Db 100 LEVQKRRIYDITNVLE-----GIGLIEKRLKNRICWKGLSVSRPGEVE 142

 Qy 142 -----WEKDQLSIK-KHDPLLREFQEG-RLLFPPTYKFDRNSNDYDTSEKKRKPAW- 191
 | | |: : | | : |: || |:| || | |
 Db 143 DEATVLQAEVDSLNL EECKLDDCIRDMQERLRIL-----SEDDRNRRWL 186

 Qy 192 --TDRILWRLKRQPCAGPDT-----PIP-----PASHFSLSLRGYSSHMT 229
 || : |: || || | | | : : || |
 Db 187 YVTDE---DIKKLPCFQNDTLIAIKAPHGTTLEVDPDEAVEYPQRRYQILLRS-----T 238

 Qy 230 YGISDHKPVSGTFDLELKPLVSAPLIV-LMPEDLWTVENDMMVSYSSSTDFP----- 280
 | | || |: : : | |:| : | : | : |
 Db 239 MGPIDVYLVS-QFEENIEEMNPVDLATELVPSGICPAEGVTISSVQEGATFVEMECQGHE 297

 Qy 281 -----SSPWDWI-GLYKVGLRDVNDYVSYAWVGDSKVSCSD----NLNQVYIDISNI 327
 : || | |: : : | | | : || | : | : : :
 Db 298 TRQPCTELTSPQDSAGGIMRIVPSDANIDADYWLLSDSGVGITDMWRTETNSTWDEVIEL 357

 Qy 328 PTTE 331
 |:
 Db 358 NPTD 361

Search completed: February 10, 2005, 18:02:13
 Job time : 25 secs

OM protein - protein search, using sw model

Run on: February 10, 2005, 17:03:41 ; Search time 166 Seconds
(without alignments)
866.716 Million cell updates/sec

Title: US-09-892-287-1
Perfect score: 2020
Sequence: 1 MDVLSPLSFIKVSHVRMQGI.....FQIPPGSLREDPLGEAQPQI 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|----------|--------------------|
| 1 | 2020 | 100.0 | 372 | 2 | AAW97094 | Aaw97094 Phosphati |
| 2 | 2020 | 100.0 | 448 | 6 | AAE36070 | Aae36070 Human pho |
| 3 | 2012 | 99.6 | 478 | 6 | AAE36067 | Aae36067 Human pho |
| 4 | 2010 | 99.5 | 372 | 6 | ABO07198 | Abo07198 Human p53 |
| 5 | 2010 | 99.5 | 372 | 6 | AAE36069 | Aae36069 Human pho |
| 6 | 2010 | 99.5 | 448 | 6 | AAE36068 | Aae36068 Human pho |
| 7 | 2010 | 99.5 | 448 | 6 | ABO53040 | Abo53040 Human put |
| 8 | 1025 | 50.7 | 240 | 8 | ADN61442 | Adn61442 Human KPP |
| 9 | 872.5 | 43.2 | 1001 | 5 | AAU98903 | Aau98903 Rat inosi |

| | | | | | | | |
|----|-------|------|------|---|----------|----------|-----------|
| 10 | 870.5 | 43.1 | 638 | 8 | ADR08504 | Adr08504 | Human pro |
| 11 | 868.5 | 43.0 | 639 | 7 | ADB65114 | Adb65114 | Human pro |
| 12 | 868.5 | 43.0 | 639 | 7 | ADM04740 | Adm04740 | Human pro |
| 13 | 868.5 | 43.0 | 1006 | 5 | AAU98904 | Aau98904 | Human ino |
| 14 | 868.5 | 43.0 | 1006 | 6 | ABU54583 | Abu54583 | Human NOV |
| 15 | 831.5 | 41.2 | 751 | 5 | AAU98902 | Aau98902 | Human ino |
| 16 | 831.5 | 41.2 | 1056 | 6 | AAE36066 | Aae36066 | Human pho |
| 17 | 683.5 | 33.8 | 279 | 4 | AAG73981 | Aag73981 | Human col |
| 18 | 637.5 | 31.6 | 254 | 6 | ABR01000 | Abr01000 | Human gen |
| 19 | 637.5 | 31.6 | 254 | 6 | ADA98192 | Ada98192 | Human sec |
| 20 | 637.5 | 31.6 | 255 | 3 | AAB27797 | Aab27797 | Human sec |
| 21 | 541.5 | 26.8 | 162 | 5 | ABP43025 | Abp43025 | Human ova |
| 22 | 507.5 | 25.1 | 508 | 4 | ABB64662 | Abb64662 | Drosophil |
| 23 | 500.5 | 24.8 | 397 | 7 | ADJ68405 | Adj68405 | Human hea |
| 24 | 494.5 | 24.5 | 381 | 3 | AAB27845 | Aab27845 | Sequence |
| 25 | 460.5 | 22.8 | 357 | 4 | ABB62704 | Abb62704 | Drosophil |
| 26 | 460.5 | 22.8 | 357 | 5 | AAU76369 | Aau76369 | Drosophil |
| 27 | 432.5 | 21.4 | 749 | 4 | AAB95181 | Aab95181 | Human pro |
| 28 | 428 | 21.2 | 382 | 3 | AAB27846 | Aab27846 | Protein f |
| 29 | 423.5 | 21.0 | 776 | 8 | ADT49828 | Adt49828 | Murine IN |
| 30 | 367.5 | 18.2 | 968 | 7 | ADJ69678 | Adj69678 | Human hea |
| 31 | 328 | 16.2 | 1244 | 7 | ADJ70439 | Adj70439 | Human hea |
| 32 | 328 | 16.2 | 1269 | 6 | ABU08111 | Abu08111 | Human kin |
| 33 | 328 | 16.2 | 1574 | 7 | ADE55582 | Ade55582 | Rat Prote |
| 34 | 328 | 16.2 | 1575 | 7 | ADE55584 | Ade55584 | Human Pro |
| 35 | 327.5 | 16.2 | 1443 | 7 | ADD46317 | Add46317 | Human Pro |
| 36 | 327.5 | 16.2 | 1443 | 7 | ADE63139 | Ade63139 | Human Pro |
| 37 | 327.5 | 16.2 | 1443 | 7 | ADJ69292 | Adj69292 | Human hea |
| 38 | 327.5 | 16.2 | 1443 | 7 | ADN95796 | Adn95796 | Human BEC |
| 39 | 327.5 | 16.2 | 1496 | 8 | ADR14671 | Adr14671 | Human NF- |
| 40 | 327.5 | 16.2 | 1496 | 8 | ABM80825 | Abm80825 | Tumour-as |
| 41 | 327.5 | 16.2 | 1510 | 5 | ABB76319 | Abb76319 | Human pro |
| 42 | 326 | 16.1 | 1248 | 7 | ADD46315 | Add46315 | Rat Prote |
| 43 | 326 | 16.1 | 1248 | 7 | ADE63137 | Ade63137 | Rat Prote |
| 44 | 316.5 | 15.7 | 1114 | 5 | AAU76370 | Aau76370 | Drosophil |
| 45 | 316.5 | 15.7 | 1218 | 4 | ABB62412 | Abb62412 | Drosophil |

ALIGNMENTS

RESULT 1

AAW97094

ID AAW97094 standard; protein; 372 AA.

XX

AC AAW97094;

XX

DT 28-APR-1999 (first entry)

XX

DE Phosphatidylinositol 4, 5-bisphosphate 5-phosphatase.

XX

KW Human; phosphatidylinositol 4,5-bisphosphate 5-phosphatase; PBPP;

KW Incyte clone 638789; antagonist; immune disorder; cancer;

KW neuronal disorder; human tubby homologue.

XX

OS Homo sapiens.

XX

| FH | Key | Location/Qualifiers |
|----|---|---|
| FT | Modified-site | 38 |
| FT | | /note= "potential phosphorylation site" |
| FT | Modified-site | 132 |
| FT | | /note= "potential phosphorylation site" |
| FT | Modified-site | 170 |
| FT | | /note= "potential phosphorylation site" |
| FT | Modified-site | 183 |
| FT | | /note= "potential phosphorylation site" |
| FT | Modified-site | 192 |
| FT | | /note= "potential phosphorylation site" |
| FT | Modified-site | 275 |
| FT | | /note= "potential phosphorylation site" |
| FT | Modified-site | 282 |
| FT | | /note= "potential phosphorylation site" |
| FT | Modified-site | 295 |
| FT | | /note= "potential phosphorylation site" |
| FT | Modified-site | 312 |
| FT | | /note= "potential phosphorylation site" |
| FT | Modified-site | 329 |
| FT | | /note= "potential phosphorylation site" |
| FT | Modified-site | 330 |
| FT | | /note= "potential phosphorylation site" |
| FT | Modified-site | 359 |
| FT | | /note= "potential phosphorylation site" |
| XX | | |
| PN | WO9900507-A1. | |
| XX | | |
| PD | 07-JAN-1999. | |
| XX | | |
| PF | 26-JUN-1998; 98WO-US013399. | |
| XX | | |
| PR | 27-JUN-1997; 97US-00884681. | |
| XX | | |
| PA | (INCY-) INCYTE PHARM INC. | |
| XX | | |
| PI | Hillman JL, Lal P, Corley NC, Shah P; | |
| XX | | |
| DR | WPI; 1999-095752/08. | |
| DR | N-PSDB; AAX15254. | |
| XX | | |
| PT | Phosphatidylinositol 4,5-bisphosphate 5-phosphatase - used for treating | |
| PT | immune disorders, cancers, and neuronal disorders. | |
| XX | | |
| PS | Claim 1; Fig 1A-G; 81pp; English. | |
| XX | | |
| CC | The present sequence encodes a human phosphatidylinositol 4,5- | |
| CC | bisphosphate 5-phosphatase (PBPP) protein. The PBPP polynucleotide was | |
| CC | first identified in Incyte clone 638789 from the breast cancer cDNA | |
| CC | library BRSTNOT03. Antagonists of the PBPP protein can be used in the | |
| CC | treatment or prevention of an immune disorder, a cancer, or a neuronal | |
| CC | disorder. The PBPP polynucleotide can be used for the detection of | |
| CC | polynucleotides encoding human tubby homologue. The immune disorders that | |
| CC | can be treated include AIDS, Addison's disease, adult respiratory | |
| CC | distress syndrome, allergies, anaemia, asthma, atherosclerosis, Crohn's | |
| CC | disease, ulcerative colitis, atopic dermatitis, gout, Grave's disease, | |
| CC | irritable bowel syndrome, lupus erythematosus, multiple sclerosis, | |

CC myasthenia gravis, osteoarthritis, osteoporosis, rheumatoid arthritis,
CC scleroderma, and autoimmune thyroiditis. Also, complications of cancer,
CC haemodialysis, extracorporeal circulation, infection, and trauma can be
CC treated using the antagonist. The neuronal disorders that can be treated
CC include Alzheimer's disease, amnesia, catatonia, amyotrophic lateral
CC sclerosis, dementia, depression, Down's syndrome, epilepsy, Huntington's
CC disease, multiple sclerosis, neurofibromatosis, Parkinson's disease,
CC paranoid psychoses, schizophrenia and Tourette's syndrome

XX

SQ Sequence 372 AA;

Query Match 100.0%; Score 2020; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 5.9e-204;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 60
      |||
Db      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 60

Qy     61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
      |||
Db     61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDIPNILDHDLIIWFGDMNFR 120

Qy    121 IEDFGLHFVRESIKNRCYGGGLEWEDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
      |||
Db    121 IEDFGLHFVRESIKNRCYGGGLEWEDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180

Qy    181 DTSEKKRKPAWTDRILWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
      |||
Db    181 DTSEKKRKPAWTDRILWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240

Qy    241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
      |||
Db    241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 300

Qy    301 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 360
      |||
Db    301 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 360

Qy    361 REDPLGEAQPQI 372
      |||
Db    361 REDPLGEAQPQI 372
```

RESULT 2

AAE36070

ID AAE36070 standard; protein; 448 AA.

XX

AC AAE36070;

XX

DT 26-JUN-2003 (first entry)

XX

DE Human phosphatidylinositol biphosphate (PIB) protein #5.

XX

KW Human; p53 pathway; phosphatidylinositol biphosphate; PIB; therapeutic;
KW cancer; apoptosis; cell proliferation; cytostatic.

XX

Db 137 KLYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 196
 Qy 121 IEDFGLHFVRESIKNRCYGGLWEKDQLSIAKKHDPLLREFQEGRLFPPTYKFDRNSNDY 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 197 IEDFGLHFVRESIKNRCYGGLWEKDQLSIAKKHDPLLREFQEGRLFPPTYKFDRNSNDY 256
 Qy 181 DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 257 DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 316
 Qy 241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 317 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY 376
 Qy 301 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 377 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 436
 Qy 361 REDPLGEAQPQI 372
 ||||||||||||
 Db 437 REDPLGEAQPQI 448

RESULT 3

AAE36067

ID AAE36067 standard; protein; 478 AA.

XX

AC AAE36067;

XX

DT 26-JUN-2003 (first entry)

XX

DE Human phosphatidylinositol biphosphate (PIB) protein #2.

XX

KW Human; p53 pathway; phosphatidylinositol biphosphate; PIB; therapeutic;

KW cancer; apoptosis; cell proliferation; cytostatic.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 56

FT /label= Unknown

XX

PN WO200299125-A1.

XX

PD 12-DEC-2002.

XX

PF 03-JUN-2002; 2002WO-US017526.

XX

PR 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0328605P.

PR 15-FEE-2002; 2002US-0357253P.

XX

PA (EXEL-) EXELIXIS INC.

XX

PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;

XX

DR WPI; 2003-167348/16.

XX
PT Identifying candidate p53 pathway-modulating agents, useful as
PT therapeutic targets for disorders associated with defective p53 function,
PT comprises screening for agents that modulate phosphatidylinositol
PT biphosphate activity.

XX
PS Claim 13; Page 128-129; 139pp; English.

XX
CC The present invention relates to a method of identifying candidate p53
CC pathway-modulating agents. The method involves screening for agents that
CC modulate the activity of phosphatidylinositol biphosphate (PIB). The
CC methods are useful for identifying candidate p53 pathway-modulating
CC agents used as therapeutic targets for disorders associated with
CC defective p53 function. They are also useful for modulating p53 pathway
CC in a mammalian cell or for diagnosing or treating a disease associated
CC with defective p53 function, e.g. cancers such as breast cancer, colon
CC cancer, lung cancer or ovarian cancer. Sequences of the invention are
CC useful for identifying and testing agents that modulate PIB function. The
CC animal models are useful for in vivo assays to test the activity of
CC candidate p53-modulating agents or to assess the role of PIB in a p53
CC pathway process such as apoptosis or cell proliferation. The present
CC sequence is human PIB protein

XX
SQ Sequence 478 AA;

Query Match 99.6%; Score 2012; DB 6; Length 478;
Best Local Similarity 99.7%; Pred. No. 6e-203;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPHYIQILSTKSTPTGLFGYWGNKGGVNICL 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 107 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPHYIQILSTKSTPTGLFGYWGNKGGVNICL 166

Qy 61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 167 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 226

Qy 121 IEDFGLHFVRESIKNRCYGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 227 IEDFGLHFVRESIKNRCYGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 286

Qy 131 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 287 DTSEKKRKPAWTDRLWLRLKRQACAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 346

Qy 241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 347 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 406

Qy 301 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 407 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 466

Qy 361 REDPLGEAQPQI 372
| | | | | | | | | |
Db 467 REDPLGEAQPQI 478

RESULT 4

ABO07198

ID ABO07198 standard; protein; 372 AA.

XX

AC ABO07198;

XX

DT 13-AUG-2003 (first entry)

XX

DE Human p53 modifying protein, SEQ ID 158.

XX

KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;

KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;

KW lung cancer; ovarian cancer; angiogenesis; cell cycle;

KW apoptotic disorder; cell proliferation disorder.

XX

OS Homo sapiens.

XX

PN WO200299122-A1.

XX

PD 12-DEC-2002.

XX

PF 03-JUN-2002; 2002WO-US017382.

XX

PR 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0328605P.

PR 15-FEB-2002; 2002US-0357253P.

XX

PA (EXEL-) EXELIXIS INC.

XX

PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;

XX

DR WPI; 2003-156859/15.

DR N-PSDB; ACD13373.

XX

PT Identifying modulators of the p53 pathway for use in treating apoptotic

PT or cell proliferation disorders, comprises screening for agents that

PT modulate activity of a human ortholog of genes that modify the p53

PT pathway in Drosophila.

XX

PS Example 2; Page 474-475; 678pp; English.

XX

CC The invention relates to identifying (M1) a candidate p53 pathway

CC modulating agent, by contacting an assay system comprising a purified HM

CC polypeptide (human orthologue of genes that modify the p53 pathway in

CC Drosophila) or nucleic acid with a test agent under conditions, where but

CC for the presence of the test agent, the system provides a reference

CC activity, and detecting a test agent-biased activity of the assay system.

CC Also included are modulating (M2) a p53 pathway of a cell (comprising

CC contacting a cell defective in p53 function with a candidate modulator

CC that specifically binds to a HM polypeptide comprising an HM amino acid

CC sequence, where p53 function is restored), modulating (M3) a p53 pathway

CC in a mammalian cell (comprising contacting the cell with an agent that

CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)

CC a disease in a patient (comprising: (a) obtaining a biological sample

CC from the patient; (b) contacting the sample with a probe for HM

CC expression; (c) comparing the results with a control; and (d) determining

CC whether the comparison indicates a likelihood disease). (M1) is useful
 CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
 CC in a patient, where the cancer has greater than 25 % expression level.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,
 CC apoptotic or cell proliferation disorders. The present sequence
 CC represents a human p53 pathway modifying protein

XX

SQ Sequence 372 AA;

Query Match 99.5%; Score 2010; DB 6; Length 372;
 Best Local Similarity 99.5%; Pred. No. 6.7e-203;
 Matches 370; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 1 | MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQLSTKSTPTGLFGYWGNGGGVNICL | 60 |
| | | | |
| Db | 1 | MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQLSTKSTPTGLFGYWGNGGGVNICL | 60 |
| Qy | 61 | KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 120 |
| | | | |
| Db | 61 | KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 120 |
| Qy | 121 | IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY | 180 |
| | | | |
| Db | 121 | IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY | 180 |
| Qy | 181 | DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 240 |
| | | | |
| Db | 181 | DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 240 |
| Qy | 241 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY | 300 |
| | | | |
| Db | 241 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY | 300 |
| Qy | 301 | VSYAWVGDSKVSCSDNLNQYIDISNIPTTEDEFLLCYYSNSLSRVVGISRPFQIPPGSL | 360 |
| | | | |
| Db | 301 | VSYAWVGDSKVSCSDNLNQYIDISNIPTTEDEFLLCYRNSLSRVVGIRRPQIPPGSL | 360 |
| Qy | 361 | REDPLGEAQPQI | 372 |
| | | | |
| Db | 361 | REDPLGEAQPQI | 372 |

RESULT 5

AAE36069

ID AAE36069 standard; protein; 372 AA.

XX

AC AAE36069;

XX

DT 25-JUN-2003 (first entry)

XX
 DE Human phosphatidylinositol biphosphate (PIB) protein #4.
 XX
 KW Human; p53 pathway; phosphatidylinositol biphosphate; PIB; therapeutic;
 KW cancer; apoptosis; cell proliferation; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200299125-A1.
 XX
 PD 12-DEC-2002.
 XX
 PF 03-JUN-2002; 2002WO-US017526.
 XX
 PR 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-0328605P.
 PR 15-FEB-2002; 2002US-0357253P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 XX
 DR WPI; 2003-167348/16.
 XX
 PT Identifying candidate p53 pathway-modulating agents, useful as
 PT therapeutic targets for disorders associated with defective p53 function,
 PT comprises screening for agents that modulate phosphatidylinositol
 PT biphosphate activity.
 XX
 PS Claim 13; Page 131-133; 139pp; English.
 XX
 CC The present invention relates to a method of identifying candidate p53
 CC pathway-modulating agents. The method involves screening for agents that
 CC modulate the activity of phosphatidylinositol biphosphate (PIB). The
 CC methods are useful for identifying candidate p53 pathway-modulating
 CC agents used as therapeutic targets for disorders associated with
 CC defective p53 function. They are also useful for modulating p53 pathway
 CC in a mammalian cell or for diagnosing or treating a disease associated
 CC with defective p53 function, e.g. cancers such as breast cancer, colon
 CC cancer, lung cancer or ovarian cancer. Sequences of the invention are
 CC useful for identifying and testing agents that modulate PIB function. The
 CC animal models are useful for in vivo assays to test the activity of
 CC candidate p53-modulating agents or to assess the role of PIB in a p53
 CC pathway process such as apoptosis or cell proliferation. The present
 CC sequence is human PIB protein
 XX
 SQ Sequence 372 AA;

Query Match 99.5%; Score 2010; DB 6; Length 372;
 Best Local Similarity 99.5%; Pred. No. 6.7e-203;
 Matches 370; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGGGVNICL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGGGVNICL 60
 Qy 61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120

| | | | | |
|----|-----|--|--|-----|
| Db | 61 | | KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 120 |
| Qy | 121 | | IEDFGLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLFPPTYKFDRNSNDY | 180 |
| Db | 121 | | IEDFGLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLFPPTYKFDRNSNDY | 180 |
| Qy | 181 | | DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 240 |
| Db | 181 | | DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 240 |
| Qy | 241 | | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVNDY | 300 |
| Db | 241 | | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVNDY | 300 |
| Qy | 301 | | VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNLSRSVVGISRPFQIPPGSL | 360 |
| Db | 301 | | VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNLSRSVVGISRPFQIPPGSL | 360 |
| Qy | 361 | | REDPLGEAQPQI | 372 |
| Db | 361 | | REDPLGEAQPQI | 372 |

RESULT 6

AAE36068

ID AAE36068 standard; protein; 448 AA.

XX

AC AAE36068;

XX

DT 26-JUN-2003 (first entry)

XX

DE Human phosphatidylinositol biphosphate (PIB) protein #3.

XX

KW Human; p53 pathway; phosphatidylinositol biphosphate; PIB; therapeutic;
 KW cancer; apoptosis; cell proliferation; cytostatic.

XX

OS Homo sapiens.

XX

PN WO200299125-A1.

XX

PD 12-DEC-2002.

XX

PF 03-JUN-2002; 2002WO-US017526.

XX

PR 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0328605P.

PR 15-FEB-2002; 2002US-0357253P.

XX

PA (EXEL-) EXELIXIS INC.

XX

PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;

XX

DR WPI; 2003-167348/16.

XX

PT Identifying candidate p53 pathway-modulating agents, useful as
 PT therapeutic targets for disorders associated with defective p53 function,

PT comprises screening for agents that modulate phosphatidylinositol
PT biphosphate activity.
XX
PS Claim 13; Page 130-131; 139pp; English.
XX
CC The present invention relates to a method of identifying candidate p53
CC pathway-modulating agents. The method involves screening for agents that
CC modulate the activity of phosphatidylinositol biphosphate (PIB). The
CC methods are useful for identifying candidate p53 pathway-modulating
CC agents used as therapeutic targets for disorders associated with
CC defective p53 function. They are also useful for modulating p53 pathway
CC in a mammalian cell or for diagnosing or treating a disease associated
CC with defective p53 function, e.g. cancers such as breast cancer, colon
CC cancer, lung cancer or ovarian cancer. Sequences of the invention are
CC useful for identifying and testing agents that modulate PIB function. The
CC animal models are useful for in vivo assays to test the activity of
CC candidate p53-modulating agents or to assess the role of PIB in a p53
CC pathway process such as apoptosis or cell proliferation. The present
CC sequence is human PIB protein
XX
SQ Sequence 448 AA;

Query Match 99.5%; Score 2010; DB 6; Length 448;
Best Local Similarity 99.5%; Pred. No. 8.9e-203;
Matches 370; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 60
      |||
Db      77 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 136

Qy      61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
      |||
Db      137 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 196

Qy      121 IEDFGLHFVRESIKNRCYGGGLEWEDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
      |||
Db      197 IEDFGLHFVRESIKNRCYGGGLEWEDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 256

Qy      181 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
      |||
Db      257 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 316

Qy      241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
      |||
Db      317 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY 376

Qy      301 VSYAWVGDSKVSCSDNLNQYIDISNIPTTEDEFLLCYYSNLSRVSVGISRPFQIPPGSL 360
      |||
Db      377 VSYAWVGDSKVSCSDNLNQYIDISNIPTTEDEFLLCYYSNLSRVSVGIRPFQIPPGSL 436

Qy      361 REDPLGEAQPQI 372
      |||
Db      437 REDPLGEAQPQI 448

```

RESULT 7
ABO53040

ID ABO53040 standard; protein; 448 AA.
XX
AC ABO53040;
XX
DT 10-OCT-2003 (first entry)
XX
DE Human putative spliceosome associated protein (SAP) #16.
XX
KW Human; SAP; spliceosome associated protein; ribonucleoprotein;
KW RNP complex; RNA affinity substrate; RNP assembly sequence;
KW spliceosomal complex; hnRNP complex; mRNA export complex;
KW mRNA localisation complex; RNA editing complex; intron complex;
KW H complex; telomerase complex; fragile X protein complex;
KW reverse transcriptase complex; gene splicing complex.
XX
OS Homo sapiens.
XX
PN US2003068803-A1.
XX
PD 10-APR-2003.
XX
PF 14-JAN-2002; 2002US-00047991.
XX
PR 12-JAN-2001; 2001US-0261521P.
XX
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
XX
PI Reed R, Zhou Z;
XX
DR WPI; 2003-540885/51.
XX
PT Isolating ribonucleoprotein complex, by contacting RNA affinity substrate
PT having ribonucleoprotein assembly sequence and affinity tag, with protein
PT mixture, subjecting complex formed to chromatography, affinity selection.
XX
PS Claim 24; Page; 39pp; English.
XX
CC The invention relates to forming (M1) an isolated ribonucleoprotein (RNP)
CC complex (C), involves contacting an RNA affinity substrate (S) comprising
CC an RNP assembly sequence (AS) and an affinity tag, with a protein mixture
CC to permit formation of (C) on AS, subjecting (C) to chromatographic
CC separation, and subjecting (C) to affinity selection, where the affinity
CC tag (e.g. bacteriophage MS2 coat protein in a fusion protein with E. coli
CC maltose binding protein) binds to an affinity matrix. Also included are
CC an isolated spliceosome preparation (isolated by (M1)), a RNA comprising
CC an RNP complex binding site and at least one phage coat protein
CC recognition site, a nucleic acid encoding the RNA, and treating (M2) a
CC subject having a disorder associated with abnormal RNP complexes (by
CC obtaining a sample of cells from a subject, purifying RNP complexes from
CC the cells of the subject by (M1), determining the presence in the
CC purified RNP complexes of one or more proteins, and normalising the
CC amount of RNPs in the subject. (M1) is useful for forming an isolated RNP
CC complex selected from a spliceosomal complex (selected from E, A, B and C
CC complex), an hnRNP complex, an mRNA export complex, an mRNA localisation
CC complex, an RNA editing complex, an intron complex, or an H complex. (M1)
CC is useful in a diagnostic assay for determining whether a subject has

CC abnormal RNP complexes, (M2) is useful for treating a subject having a
 CC disorder associated with abnormal RNP complexes. (M1) is useful for
 CC forming an isolated RNP complex such as a telomerase complex, a fragile X
 CC protein complex, a reverse transcriptase complex or a gene splicing
 CC complex. The present sequence represents a putative novel human
 CC spliceosome associated protein (SAP) isolated by the methods of the
 CC invention. Note: The present sequence is not shown in the specification
 CC but was obtained from Genbank or Swissprot using the information provided
 CC in table 2 of the specification
 XX
 SQ Sequence 448 AA;

Query Match 99.5%; Score 2010; DB 6; Length 448;
 Best Local Similarity 99.5%; Pred. No. 8.9e-203;
 Matches 370; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

| | | | | | | | |
|----|-----|---------------|-------------|---------------|--------------|---------------------|----------------|
| Qy | 1 | MDVLSPLSFIKVS | HVRMQGILLLV | FAKYQHLPYIQIL | STKSTPTGLFGY | WGNKGGVNICL | 60 |
| | | | | | | | |
| Db | 77 | MDVLSPLSFIKVS | HVRMQGILLLV | FAKYQHLPYIQIL | STKSTPTGLFGY | WGNKGGVNICL | 136 |
| Qy | 61 | KLYGYYVSIINCH | LPPHISNNYQR | LEHFDRIEMQN | CEGRDIPNILD | HDLIIWFGDMNFR | 120 |
| | | | | | | | |
| Db | 137 | KLYGYYVSIINCH | LPPHISNNYQR | LEHFDRIEMQN | CEGRDIPNILD | HDLIIWFGDMNFR | 196 |
| Qy | 121 | IEDFGLHFVRESI | KNRCYGGWLEK | DQLSIAKKHDPL | LLREFQEGRL | LPPTYKFDRNSNDY | 130 |
| | | | | | | | |
| Db | 197 | IEDFGLHFVRESI | KNRCYGGWLEK | DQLSIAKKHDPL | LLREFQEGRL | LPPTYKFDRNSNDY | 256 |
| Qy | 181 | DTSEKKRKP | AWTDRI | LWRLKRQPCAG | PDTPIPPASHF | SLSLRGYSSHMTY | GISDHKPVSG 240 |
| | | | | | | | |
| Db | 257 | DTSEKKRKP | AWTDRI | LWRLKRQPCAG | PDTPIPPASHF | SLSLRGYSSHMTY | GISDHKPVSG 316 |
| Qy | 241 | TFDLELKPLVS | APLIVLMPED | LWTVENDMMV | SYSSTSDFPSS | PWDWIGLYKVGLRDVNDY | 300 |
| | | | | | | | |
| Db | 317 | TFDLELKPLVS | APLIVLMPED | LWTVENDMMV | SYSSTSDFPSS | PWDWIGLYKVGLRDVNDY | 376 |
| Qy | 301 | VSYAWVGDSKV | SCSDNLNQVY | IDISNIPTTE | DEFLLCYYSN | SLRSVVGISRPFQIPPGSL | 360 |
| | | | | | | | |
| Db | 377 | VSYAWVGDSKV | SCSDNLNQVY | IDISNIPTTE | DEFLLCYYSN | SLRSVVGISRPFQIPPGSL | 436 |
| Qy | 361 | REDPLGEAQPQI | | | | | 372 |
| | | | | | | | |
| Db | 437 | REDPLGEAQPQI | | | | | 448 |

RESULT 8

ADN61442

ID ADN61442 standard; protein; 240 AA.

XX

AC ADN61442;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human KPP-8 protein SEQ ID NO:8.

XX

KW human; kinase; phosphatase; enzyme; KPP; cytostatic;

KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;

KW cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
 KW thyromimetic; gene therapy; cell proliferative disorder; cancer;
 KW atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
 KW stroke; immune disorder; inflammatory disorder; AIDS; allergy;
 KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection.
 XX
 OS Homo sapiens.
 XX
 PN WO2004042022-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034809.
 XX
 PR 01-NOV-2002; 2002US-0423226P.
 PR 15-NOV-2002; 2002US-0426713P.
 PR 26-NOV-2002; 2002US-0429766P.
 PR 11-FEB-2003; 2003US-0447043P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Hafalia AJA, Lee S, Murage J, Swarnakar A, Chawla NK, Khare R;
 PI Elliott VS, Tran UK, Ramkumar J, Gururajan R, Baughn MR, Gietzen KJ;
 PI Yang YG, Chien D, Wang JT, Favero KD, Becha SD, Richardson TW;
 PI Jin P, Hawkins PR, Yue H, Lee EA, Marquis JP;
 XX
 DR WPI; 2004-390608/36.
 DR N-PSDB; ADN61498.
 XX
 PT New human kinases and phosphatases (KPP), useful for diagnosing, treating
 PT and preventing diseases or conditions associated with the aberrant KPP
 PT expression e.g. cancer, AIDS, epilepsy, or infections.
 XX
 PS Claim 1; SEQ ID NO 8; 320pp; English.
 XX
 CC The present sequence represents a human kinase and phosphatase protein
 CC designated KPP-8. Human KPP sequences have cytostatic,
 CC antiarteriosclerotic, anticonvulsant, nootropic, neuroprotective,
 CC cerebroprotective, anti-HIV, antiallergic, antiinflammatory and
 CC thyromimetic activities, and can be used in gene therapy. The human KPP
 CC polypeptides and polynucleotides of the invention are useful in
 CC diagnosing, treating and preventing diseases or conditions associated
 CC with the decreased expression or overexpression of KPP, such as cell
 CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
 CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
 CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
 CC disorders, or infections. They are also useful in assessing the effects
 CC of exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of KPP. The KPP sequences or their fragments are useful in
 CC screening compounds for effectiveness as agonist or antagonist of the
 CC polypeptides, or in altering the expression of the target polynucleotide
 CC and compounds that specifically bind to or modulate the activity of the
 CC polypeptide.
 XX
 SQ Sequence 240 AA;

Query Match

50.7%; Score 1025; DB 8; Length 240;

Best Local Similarity 97.0%; Pred. No. 3.6e-99;
Matches 191; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

Qy      176 NSNDYDTSEKKRKPAWTDRLWRLKRPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDH 235
      | : | |||||
Db      44 NLDIYVIGEKKRKPAWTDRLWRLKRPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDH 103

Qy      236 KPVSGTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLR 295
      |||||
Db      104 KPVSGTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLR 163

Qy      296 DVNDYVSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQI 355
      |||||
Db      164 DVNDYVSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQI 223

Qy      356 PPGSLREDPLGEAQPQI 372
      |||||
Db      224 PPGSLREDPLGEAQPQI 240

```

RESULT 9

AAU98903

ID AAU98903 standard; protein; 1001 AA.

XX

AC AAU98903;

XX

DT 22-AUG-2002 (first entry)

XX

DE Rat inositol polyphosphate 5-phosphatase.

XX

KW Human; inositol polyphosphate 5-phosphatase; asthma; diabetes;

KW chronic obstructive pulmonary disease; cancer; enzyme.

XX

OS Rattus norvegicus.

XX

PN WO200236755-A2.

XX

PD 10-MAY-2002.

XX

PF 29-OCT-2001; 2001WO-EP012496.

XX

PR 30-OCT-2000; 2000US-0243745P.

PR 26-DEC-2000; 2000US-0257302P.

PR 27-AUG-2001; 2001US-0314660P.

XX

PA (FARB) BAYER AG.

XX

PI Kossida S;

XX

DR WPI; 2002-490008/52.

XX

PT New human inositol polyphosphate 5-phosphate polypeptide, useful for
PT treating chronic obstructive pulmonary disease, asthma, diabetes or
PT cancer.

XX

PS Disclosure; Fig 3; 135pp; English.

XX

CC The invention relates to novel purified human inositol polyphosphate 5-
CC phosphatase polypeptide (I) and the polynucleotide (II) encoding it. (I)
CC and (II) are useful for screening for agents which decrease the activity
CC of human inositol polyphosphate 5-phosphatase polypeptide. (I) or (II)
CC are also useful for screening for agents which modulate the activity of
CC human inositol polyphosphate 5-phosphatase. A reagent that modulates (I)
CC or (II) is useful for treating a human inositol polyphosphate 5-
CC phosphatase dysfunction related disease, such as chronic obstructive
CC pulmonary disease, asthma, diabetes or cancer. The present sequence
CC represents rat inositol polyphosphate 5- phosphatase

XX

SQ Sequence 1001 AA;

Query Match 43.2%; Score 872.5; DB 5; Length 1001;
Best Local Similarity 47.5%; Pred. No. 4.2e-82;
Matches 169; Conservative 56; Mismatches 126; Indels 5; Gaps 4;

QY 1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNKGGVNICL 60
|| | | :|: || |||||:|:| ||| |||:|: | | ||| |||||:|:| |
Db 483 MDALGPFNFVLVSTVRMQGVILLVFAKYHLPFLRDVQTDCTRTGLGGYWGNKGGVSVRL 542

QY 61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
:|: : :| |||| | : || :| || :| |||||: |||: |||
Db 543 AAFGHMLCFLNCHLPAHMDKAEQRKDNFQTILSLQQFQGPAGHILDHDLVFWFGDLNFR 602

QY 121 IEDFGLHFVRESIKNRCYGGWLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
|| : ||||: :| : |||||:| ||| :|: |||| | | ||: ||| :| |
Db 603 IESYDLHFVKFAIDSNQLHQLWEKDQLNMAKNTWPILKGFQEGPLNFAPTFKFDVGTNKY 662

QY 131 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPVS 239
||| ||||| |||||:| | || :| || :| ||| | :||| ||:|
Db 663 DTSAKKRKPAWTDRLWKVK-APSGGP-SPSGRESHRLQVTQHSYRSHMEYTVSDHKPVA 720

QY 240 GTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVND 299
| |: ||: | || :| | : | | |||||: || | |
Db 721 ARFLLQFAFRDDVPLVRLEVADEWARPEQAVVRYRVETVVFARSSWDWIGLYRVGFRHCKD 780

QY 300 YVSYAWVGDSKVS CSDNLNQYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQI 355
||:| | :| | : || :| :|: |||: :|: |||
Db 781 YVAYVWAKHEEV--DGNIIYQVTFSEESLPKGGHGFILGYSHHHSILIGVTEPFQI 834

RESULT 10

ADR08504

ID ADR08504 standard; protein; 638 AA.

XX

AC ADR08504;

XX

DT 04-NOV-2004 (first entry)

XX

DE Human protein useful for treating neurological disease Seq 2010.

XX

KW human; oligo-capping method; diagnostic marker; gene therapy;

KW osteoporosis; neurological disease; Alzheimer's disease;

KW Parkinson's disease; dementia; short memory; cancer;

KW sense or motor function; emotional reaction; fear response; panic;

KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;

KW tranquiliser.
 XX
 OS Homo sapiens.
 XX
 PN EP1447413-A2.
 XX
 PD 18-AUG-2004.
 XX
 PF 12-FEB-2004; 2004EP-00003145.
 XX
 PR 14-FEB-2003; 2003JP-00102207.
 PR 09-MAY-2003; 2003JP-00131452.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
 PI Wakamatsu A, Ishii S, Nagai K, Irie R;
 XX
 DR WPI; 2004-583265/57.
 DR N-PSDB; ADR06548.
 XX
 PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX
 PS Claim 1; SEQ ID NO 2010; 2686pp; English.
 XX
 CC This invention relates to novel, isolated full length human cDNA
 CC molecules and the encoded proteins thereof. Specifically, it refers to
 CC cDNA clones obtained by an oligo-capping method, where none of these
 CC clones are identical to any known human mRNAs. The present invention
 CC describes an immunoassay to identify agonists and antagonists, as well as
 CC antibodies, antisense molecules and siRNAs that can all be used to bind
 CC to and modulate expression of the cDNA molecules. As such, these
 CC molecules are useful for diagnostic markers or therapeutic targets for
 CC the various diseases or morbid states. In particular, they are useful in
 CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
 CC disease, Parkinson's disease, dementia, short memory and various cancers,
 CC as well as for maintaining equilibrium of sense or motor function, and
 CC for treating emotional reaction, fear response and panic. Accordingly,
 CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
 CC cytostatic and tranquiliser activities. This polypeptide is a protein
 CC encoded by a full length human cDNA sequence of the invention. NOTE: This
 CC sequence is not given in the sequence listing of the specification but
 CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
 CC office.
 XX
 SQ Sequence 638 AA;

Query Match 43.1%; Score 870.5; DB 8; Length 638;
 Best Local Similarity 47.8%; Pred. No. 3.4e-82;
 Matches 170; Conservative 54; Mismatches 127; Indels 5; Gaps 4;

Qy 1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQLSTKSTPTGLFGYWGNGKGGVNICL 60
 || || | :|: || |||||:|:| ||| | | | | | | | | :|
 Db 120 MDALGPFNFVLVSSVRMQGVILLLVFAKYHLPFLRDVQTDCTRTGLGGYWGNGKGGVSVRL 179
 Qy 61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDIPNILDHDLIIWFGDMNFR 120

```

      :|: : :| ||| | : || :| || :| :| |||||: |||: |||
Db      180 AAFGHMLCFLNCHLPAHMDKAEQRKDNFQTILSLQQFQGPQAQGILDHDLVFWFGDLNFR 239
Qy      121 IEDFGLHFVRESIKNRCYGGWLWEKDQLSIAKKHDPLLREFQEGRLFPPTYKFDRNSNDY 180
      || : ||||: :| : |||||:| ||| :|: |||| | | ||: ||| :| |
Db      240 IESYDLHFVKFAIDSDQLHQLWEKDQLNMAKNTWPILKGFQEGPLNFAPTFFKFDAGTNKY 299
Qy      181 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPV 239
      ||| ||||| |||||:| | || :| || :| :| ||| | :||| ||:
Db      300 DTSAKRKPAWTDRLWKVK-APGGGP-SPSGRKSHRLQVTQHSYRSHMEYTVSDHKPVA 357
Qy      240 GTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVND 299
      | |: ||: | | | :| | :| | |||||: || | |
Db      358 AQFLLQFAFRDDMPLVRLEVADEWVRPEQAVVRYRMETVFARSSWDWIGLYRVGFRHCKD 417
Qy      300 YVSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQI 355
      ||:| | | | || :| :|: |||: :||: |||
Db      418 YVAYVWAKHEDV--DGNTYQVTFSEESLPKGGHGFILGYSHNHSILIGITEPFQI 471

```

RESULT 11

ADB65114

ID ADE65114 standard; protein; 639 AA.

XX

AC ADB65114;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human protein encoded by clone SPLEN20024930.

XX

KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.

XX

OS Homo sapiens.

XX

PN EP1308459-A2.

XX

PD 07-MAY-2003.

XX

PF 28-MAR-2002; 2002EP-00007401.

XX

PR 05-NOV-2001; 2001JP-00379298.

PR 25-JAN-2002; 2002US-00350978.

XX

PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX

DR WPI; 2003-450961/43.

DR N-PSDB; ADB63144.

XX

PT New polynucleotides and polypeptides, useful for developing a diagnostic

Db ||:| | | || ::| :::| |||:: ::||: ||||
419 YVAYVWAKHEDV--DGNTYQVTFSEESLPKGGHDFILGYYSNHSILIGITEPFQI 472

RESULT 12

ADM04740

ID ADM04740 standard; protein; 639 AA.

XX

AC ADM04740;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human protein of the invention SEQ ID NO:3425.

XX

KW human; gene therapy; diagnostic marker; pharmaceutical.

XX

OS Homo sapiens.

XX

PN EP1347046-A1.

XX

PD 24-SEP-2003.

XX

PF 12-APR-2002; 2002EP-00008400.

XX

PR 22-MAR-2002; 2002JP-00137785.

XX

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX

DR WPI; 2003-723553/69.

DR N-PSDB; ADM02297.

XX

PT New polynucleotides and polypeptides are useful in gene therapy, for

PT developing a diagnostic marker or medicines for regulating their

PT expression and activity, or as a target of gene therapy.

XX

PS Claim 1; SEQ ID NO 3425; 305pp; English.

XX

CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.

XX

SQ Sequence 639 AA;

Query Match 43.0%; Score 868.5; DB 7; Length 639;

Best Local Similarity 47.8%; Pred. No. 5.6e-82;

Matches 170; Conservative 54; Mismatches 127; Indels 5; Gaps 4;

Qy 1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 60
 || | | :|: || |||||:|:| ||| |||: : | | ||| ||||| |||:|
 Db 121 MDALGPFNFVLVSSVRMQGVILLVFAKYHLPFLRDVQTDCTRTGLGGYWGNGGGVSVRL 180

Qy 61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
 :|: : : ||||| | : || :| || :| :| |||||: |||: |||
 Db 181 AAFGHMLCFLNCHLPAHMDKAEQRKDNFQTILSLQQFQGPGAQGILDHDLVFWFGDLNFR 240

Qy 121 IEDFGLHFVRESIKNRCYGGWLEKDQLSIAKKHDPDLLREFQEGRLFPPTYKFDRNSNDY 180
 || : ||||: :| : |||||:| ||| :|: |||| | | ||: ||| :| |
 Db 241 IESYDLHFVKFAIDSDQLHQLWEKDQLNMAKNTWPILKGFQEGPLNFAPTFKFDVGTNKY 300

Qy 181 DTSEKKRKPAWTDRLWLKRQPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPV 239
 ||| ||||| |||||:| | || :| || :| :| ||| | :||| |||:
 Db 301 DTSAKKRKPAWTDRLWKVK-APGGGP-SPSGRKSHRLQVTQHSYRSHMEYTVSDHKPVA 358

Qy 240 GTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVND 299
 | |: ||: | | | :| | : | | |||||: || | |
 Db 359 AQFLLQFAFRDDMPLVRLEVADEWVRPEQAVVRYRMETVFARSSWDWIGLYRVGFRHCKD 418

Qy 300 YVSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNLSRVS VGISRPFI 355
 ||:| | | | | || :| :|: |||: :|: |||
 Db 419 YVAYVWAKHEDV--DGNTYQVTFSEESLPKGGHDFILGYYSNHSILIGITEPFI 472

RESULT 13

AAU98904

ID AAU98904 standard; protein; 1006 AA.

XX

AC AAU98904;

XX

DT 22-AUG-2002 (first entry)

XX

DE Human inositol polyphosphate 5-phosphatase #2.

XX

KW Human; inositol polyphosphate 5-phosphatase; asthma; diabetes;

KW chronic obstructive pulmonary disease; cancer; enzyme.

XX

OS Homo sapiens.

XX

PN WO200236755-A2.

XX

PD 10-MAY-2002.

XX

PF 29-OCT-2001; 2001WO-EP012496.

XX

PR 30-OCT-2000; 2000US-0243745P.

PR 26-DEC-2000; 2000US-0257302P.

PR 27-AUG-2001; 2001US-0314660P.

XX

PA (FARB) BAYER AG.

XX

PI Kossida S;

XX

DR WPI; 2002-490008/52.

DR N-PSDB; ABK86166.

XX
PT New human inositol polyphosphate 5-phosphate polypeptide, useful for
PT treating chronic obstructive pulmonary disease, asthma, diabetes or
PT cancer.
XX
PS Claim 25; Fig 12; 135pp; English.
XX
CC The invention relates to novel purified human inositol polyphosphate 5-
CC phosphatase polypeptide (I) and the polynucleotide (II) encoding it. (I)
CC and (II) are useful for screening for agents which decrease the activity
CC of human inositol polyphosphate 5-phosphatase polypeptide. (I) or (II)
CC are also useful for screening for agents which modulate the activity of
CC human inositol polyphosphate 5-phosphatase. A reagent that modulates (I)
CC or (II) is useful for treating a human inositol polyphosphate 5-
CC phosphatase dysfunction related disease, such as chronic obstructive
CC pulmonary disease, asthma, diabetes or cancer. The present sequence
CC represents human inositol polyphosphate 5- phosphatase
XX
SQ Sequence 1006 AA;

Query Match 43.0%; Score 868.5; DB 5; Length 1006;
Best Local Similarity 47.8%; Pred. No. 1.1e-81;
Matches 170; Conservative 54; Mismatches 127; Indels 5; Gaps 4;

Qy 1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 60
| | | | : | | | | | : | | | | | | : | | | | | | : |
Db 48E MDALGPFNFVLVSSVRMQGVIIILLFAKYYHLPFLRDVQTDCTRTGLGGYWGNGGGVSVRL 547
Qy 61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
: | : : : | | | | | : | | : | | : | | | | : | | | : | |
Db 548 AAFGHMLCFLNCHLPAHMDKAEQRKDNFQTILSLQQFQGPQAQGILDHDLVFWFGDLNFR 607
Qy 121 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLFPPTYKFDRNSNDY 180
| | : | | | : : | : | | | | | : | | | : | | | | : | |
Db 608 IESYDLHFVKFAIDSDQLHQLWEKDQLNMAKNTWPILKGFQEGPLNFAPTFKFDVGTNKY 667
Qy 181 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPV 239
| | | | | | | | | | : | | | : | | : : | | | | : | | | :
Db 668 DTSAKKRKPAWTDRIWKVK-APGGGP-SPSGRKSHRLQVTQHSYRSHMEYTVSDHKPVA 725
Qy 240 GTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVND 299
| | : | | : | | : | | : | | | | | : | | | | |
Db 726 AQFLLQFAFRDDMPLVRLEVADEWVRPEQAVVRYRMETVFARSSWDWIGLYRVGFRHCKD 785
Qy 300 YVSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQI 355
| | : | | | | | | | : | : | | : | | : | : | : | | |
Db 786 YVAYVWAKHEDV--DGNTYQVTFSEESLPKGGHGFILGYYSHNHSILIGITEPFQI 839

RESULT 14
ABU54583
ID ABU54583 standard; protein; 1006 AA.
XX
AC ABU54583;
XX
DT 03-JUN-2003 (first entry)
XX

DE Human NOVX polypeptide #42.
 XX
 KW Human; NOVX; metabolic disorder; cardiomyopathy; diabetes; ASD;
 KW hypertension; congenital heart defect; aortic stenosis; valve disease;
 KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
 KW pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;
 KW tuberous sclerosis; scleroderma; atherosclerosis; infectious disease;
 KW obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;
 KW Parkinson's disease; immune disorder; haematopoietic disorder;
 KW haemophilia; hypercoagulation; Crohn's disease; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200281498-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010780.
 XX
 PR 03-APR-2001; 2001US-0281086P.
 PR 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 06-APR-2001; 2001US-0282020P.
 PR 10-APR-2001; 2001US-0282930P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 12-APR-2001; 2001US-0283512P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285381P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0285890P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 25-APR-2001; 2001US-0286292P.
 PR 27-APR-2001; 2001US-0287213P.
 PR 02-MAY-2001; 2001US-0288257P.
 PR 29-MAY-2001; 2001US-0294164P.
 PR 30-MAY-2001; 2001US-0294484P.
 PR 18-JUN-2001; 2001US-0298952P.
 PR 19-JUN-2001; 2001US-0299237P.
 PR 19-JUN-2001; 2001US-0299276P.
 PR 12-SEP-2001; 2001US-0318750P.
 PR 25-SEP-2001; 2001US-0324800P.
 PR 25-SEP-2001; 2001US-0324802P.
 PR 27-SEP-2001; 2001US-0325684P.
 PR 17-OCT-2001; 2001US-0330143P.
 PR 14-NOV-2001; 2001US-0332131P.
 PR 14-NOV-2001; 2001US-0332240P.
 PR 14-NOV-2001; 2001US-0332779P.
 PR 21-NOV-2001; 2001US-0332115P.
 PR 04-DEC-2001; 2001US-0337621P.
 PR 03-JAN-2002; 2002US-0345783P.
 PR 16-JAN-2002; 2002US-0350251P.
 PR 02-APR-2002; 2002US-00114270.
 XX

PA (CURA-) CURAGEN CORP.

PI Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;
PI Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD;
PI Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Gerlach V;
PI Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ, Ji W;
PI Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
PI Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;
PI Ellerman K;

DR WPI; 2003-046858/04.

DR N-PSDB: ABX72211.

PT New isolated NOVX polypeptide useful for treating atherosclerosis,
PT metabolic disorders, diabetes, obesity, infectious disease, anorexia,
PT neurodegenerative disorders, Alzheimer's disease and cancer.

PS Claim 1; Page 179-180; 666pp; English.

CC The invention relates to human polypeptides, termed NOVX, and the
CC polynucleotides encoding them. The polypeptides and polynucleotides are
CC useful for diagnosing disease, and screening for potential therapeutic
CC agents. The sequences are useful for treating metabolic disorders,
CC cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic
CC stenosis, atrial septal defect (ASD), atrioventricular canal defect,
CC ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
CC septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma,
CC atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
CC and cancer. Sequences ABU54542-ABU54647 represent human NOVX polypeptides
CC of the invention

XX
SQ Sequence 1006 AA;

Query Match 43.0%; Score 868.5; DB 6; Length 1006;
Best Local Similarity 47.8%; Pred. No. 1.1e-81;
Matches 170; Conservative 54; Mismatches 127; Indels 5; Gaps 4;

QY 1 MDVLSPLSFIKVSHVRMQGILLVFAKYQHLPIYIQILSTKSTPTGLFGYWGNKGGVNICL 60
||| :|: |||||::||:|||| |||:: : | | ||| ||||| |||:: |
Db 438 MDAIGPENEVLVSSVRMOGVILLLEAKYYHLPELRDVTDCRTTGLGGYWGNKGGVSVRL 547

Qy 61 KLYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
:|: : :||| | : || :| || :| :| |||||: |||:| |
Db 548 AAFGHMLCFLNCHLPAHMDKAEORKDNFOTILSLOOFOGPGAOGILDHDLVFWFGDLNFR 607

Db 548 AAFGHMLCFLNCHLPAHMDKAEQRKDNFQTIISLQQFQGPGAQGILDHDLVFWFGDLNFR 607

Ov 121 IEDFGLHFVRESIKNRCYGGLEWKDOLSIKKHDPDLLREFOEGRLLFPPTYKFDNRNSNDY 180

Qy 121 IEDFGLHFVRESIKNRCYGGLEWKDQLSIAKKHDPDLLREFQEGRLLPPTYKFDRNSNDY 180
|| : ||||: :| : |||||:| || :|: |||| | | ||:| | :| |
Db 603 IESYDLHFVKFAIDSDOLHOLWEKDOLNMAKNTWPILKGFQEGPLNFAPTFFKFDVGTNKY 667

QY 181 DTSEKKRKPAWTDRILWRLKRPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPV 239
||| ||||| ||||| ::| | || :| || :: | ||| | :||| | :
Db 668 DTSAKRKPAWTDRILWKVK-APGGGP-SPSGRKRSHRLOVTOHSYRSHMEYTVSDHKPVA 725

Db 668 DTSAKKRKPAWTDRILWKVK-APGGGP-SPSGRKSHRLQVTQHSYRSHMEYTVSDHKPVA 725

Ov 240 GTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDPEPSPWDWIGLYKVGRLRDVND 299

QY 240 GTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVND 299

| | | | | |
|----|--|-----|---|-----|
| Db | | 726 | AQFLLQFAFRDDMPLVRLEVADEWVWRPEQAVVRYRMETVFARSSWDWGILYRVGFRHCKD | 785 |
| Qy | | 300 | YVS YAWVGDSK VSCSDNLNQVI IDISNIPTTEDEF LLCCYYNSNLSR SVVGISRPFQI | 355 |
| | | | : :: : : : :: : : | |
| Db | | 786 | YVAYVWAKHEDV--DGNTYOVT FSEESLPKGHGDF ILGYYSNHHS I LIGITEPFOI | 839 |

RESULT 15

AAU98902

ID AAU98902 standard; protein; 751 AA.

XX

AC AAU98902;

XX

DT 22-AUG-2002 (first entry)

XX

DE Human inositol polyphosphate 5-phosphatase #1.

XX

KW Human; inositol polyphosphate 5-phosphatase; asthma; diabetes;

KW chronic obstructive pulmonary disease; cancer; enzyme.

XX

OS Hcmo sapiens.

XX

PN WO200236755-A2.

XX

PD 10-MAY-2002.

XX

PF 29-OCT-2001; 2001WO-EP012496.

XX

PR 30-OCT-2000; 2000US-0243745P.

PR 26-DEC-2000; 2000US-0257302P.

PR 27-AUG-2001; 2001US-0314660P.

XX

PA (FARB) BAYER AG.

XX

PI Kossida S;

XX

DR WPI; 2002-490008/52.

DR N-PSDB; ABK86158.

XX

PT New human inositol polyphosphate 5-phosphate polypeptide, useful for

PT treating chronic obstructive pulmonary disease, asthma, diabetes or

PT cancer.

XX

PS Claim 25; Fig 2; 135pp; English.

XX

CC The invention relates to novel purified human inositol polyphosphate 5-
CC phosphatase polypeptide (I) and the polynucleotide (II) encoding it. (I)
CC and (II) are useful for screening for agents which decrease the activity
CC of human inositol polyphosphate 5-phosphatase polypeptide. (I) or (II)
CC are also useful for screening for agents which modulate the activity of
CC human inositol polyphosphate 5-phosphatase. A reagent that modulates (I)
CC or (II) is useful for treating a human inositol polyphosphate 5-
CC phosphatase dysfunction related disease, such as chronic obstructive
CC pulmonary disease, asthma, diabetes or cancer. The present sequence
CC represents a human inositol polyphosphate 5- phosphatase

XX

SQ Sequence 751 AA;

Query Match 41.2%; Score 831.5; DB 5; Length 751;
 Best Local Similarity 42.9%; Pred. No. 5.8e-78;
 Matches 169; Conservative 56; Mismatches 126; Indels 43; Gaps 6;

```

Qy      1 MDVLSPLSFIKVSH-----VRMQGILLLVFA 26
      || | | :|: |:|
Db      195 MDALGPFNFVLVTHPSPPGQPETLLNSWLQLYPGSLWGPLGLCGWVSSVRMQGVILLLFA 254

Qy      27 KYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICKLYGYVSIINCHLPPHISNNYQRLE 86
      || |||::: : | | ||| |||||::: | :|: : : ||||| |: || :
Db      255 KYYHLPFLRDVQTDCTRTGLGGYWGNGGGVSVRLAAFGHMLCFLNCHLPAHMDKAEQRKD 314

Qy      87 HFDRILEMQNCEGRDIPNILDHD---LIIWFGDMNFRIEDFGLHFVRESIKNRCYGGGLW 142
      :| || :| :| ||||: |: ||||:||||| : ||||: :| : ||
Db      315 NFQTILSLQQFQGPQAQGILDHEYGLGLVFWFGDLNFRIESYDLHFVKFAIDSDQLHQLW 374

Qy     143 EKDQLSIAKKHDPLLREFQEGRLLPPTYKFDNRNSNDYDTSEKKRKPAWTDRLWLKLRQ 202
      |||||::|| |:|: |||| | | ||:|||| :| |||| |||||:::|
Db      375 EKDQLNMAKNTWPILKGFQEGPLNFAPTFKFDVGTNKYDTSAKKRKPAWTDRLWKVK-A 433

Qy     203 PCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPVSGTFDLELKPLVSAPLIVLMPED 261
      | || :| || :| | || | :|||::: | |: ||: | |
Db      434 PGGGP-SPSGRKSHRLQVTQHSYRSHMEYTVSDHKPVAAQFLLQFAFRDDMPLVRLEVAD 492

Qy     262 LWTVENDDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVNDYVSYAWVGDSKVSCSDNLNQVY 321
      | :| | :| | |||||::| | ||:| | | | ||
Db      493 EWRPEQAVVRYRMETVFARSSWDWIGLYRVGFRHCKDYVAYVWAKHEDV--DGNTYQVT 550

Qy     322 IDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQI 355
      ::| :|:| |||:: :|:| |||
Db      551 FSEESLPKGHGDFILGYYSNHSILIGITEPFQI 584
  
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Search completed: February 10, 2005, 17:49:57
 Job time : 170 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 17:50:07 ; Search time 43 Seconds
 (without alignments)
 645.801 Million cell updates/sec

Title: US-09-892-287-1
 Perfect score: 2020
 Sequence: 1 MDVLSPLSFIKVSHVRMQGI.....FQIPPGSLREDPLGEAQFQI 372

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---------------|-------|---------------------|--------|----|----------------------|-------------------|
| 1 | 2020 | 100.0 | 372 | 2 | US-08-884-681-1 | Sequence 1, Appli |
| 2 | 2020 | 100.0 | 372 | 3 | US-09-258-643-1 | Sequence 1, Appli |
| 3 | 1791 | 88.7 | 329 | 2 | US-08-884-681-3 | Sequence 3, Appli |
| 4 | 1791 | 88.7 | 329 | 3 | US-09-258-643-3 | Sequence 3, Appli |
| 5 | 432.5 | 21.4 | 942 | 2 | US-08-884-681-4 | Sequence 4, Appli |
| 6 | 432.5 | 21.4 | 942 | 3 | US-08-560-005-6 | Sequence 6, Appli |
| 7 | 432.5 | 21.4 | 942 | 3 | US-09-258-643-4 | Sequence 4, Appli |
| 8 | 432.5 | 21.4 | 942 | 3 | US-09-418-540-6 | Sequence 6, Appli |
| 9 | 432.5 | 21.4 | 942 | 4 | US-09-969-528-6 | Sequence 6, Appli |
| 10 | 368.5 | 18.2 | 968 | 3 | US-08-560-005-7 | Sequence 7, Appli |
| 11 | 368.5 | 18.2 | 968 | 3 | US-09-418-540-7 | Sequence 7, Appli |
| 12 | 368.5 | 18.2 | 968 | 4 | US-09-969-528-7 | Sequence 7, Appli |
| 13 | 367.5 | 18.2 | 901 | 2 | US-08-884-681-5 | Sequence 5, Appli |
| 14 | 367.5 | 18.2 | 901 | 3 | US-09-258-643-5 | Sequence 5, Appli |
| 15 | 367.5 | 18.2 | 952 | 4 | US-09-949-016-7283 | Sequence 7283, Ap |
| 16 | 367.5 | 18.2 | 952 | 4 | US-09-949-016-7284 | Sequence 7284, Ap |
| 17 | 328 | 16.2 | 350 | 4 | US-09-248-796A-18330 | Sequence 18330, A |
| 18 | 328 | 16.2 | 1587 | 4 | US-09-949-016-11062 | Sequence 11062, A |
| 19 | 324.5 | 16.1 | 818 | 4 | US-09-248-796A-18342 | Sequence 18342, A |
| 20 | 290.5 | 14.4 | 946 | 3 | US-08-560-005-4 | Sequence 4, Appli |
| 21 | 290.5 | 14.4 | 946 | 3 | US-09-418-540-4 | Sequence 4, Appli |
| 22 | 290.5 | 14.4 | 946 | 4 | US-09-969-528-4 | Sequence 4, Appli |
| 23 | 287 | 14.2 | 1149 | 3 | US-08-560-005-5 | Sequence 5, Appli |
| 24 | 287 | 14.2 | 1149 | 3 | US-09-418-540-5 | Sequence 5, Appli |
| 25 | 287 | 14.2 | 1149 | 4 | US-09-969-528-5 | Sequence 5, Appli |
| 26 | 284 | 14.1 | 1254 | 4 | US-09-949-016-7777 | Sequence 7777, Ap |
| 27 | 264 | 14.1 | 1258 | 4 | US-09-922-543-1 | Sequence 1, Appli |
| 28 | 263 | 13.0 | 654 | 3 | US-08-560-005-10 | Sequence 10, Appl |
| 29 | 263 | 13.0 | 654 | 3 | US-09-418-540-10 | Sequence 10, Appl |
| 30 | 263 | 13.0 | 654 | 4 | US-09-969-528-10 | Sequence 10, Appl |
| 31 | 252 | 12.5 | 968 | 1 | US-08-434-730-14 | Sequence 14, Appl |
| 32 | 251 | 12.4 | 1185 | 3 | US-08-664-962B-2 | Sequence 2, Appli |

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|----|-------|------|------|---|---------------------|-------------------|
| 33 | 251 | 12.4 | 1185 | 3 | US-09-311-743-2 | Sequence 2, Appli |
| 34 | 250 | 12.4 | 976 | 3 | US-08-560-005-2 | Sequence 2, Appli |
| 35 | 250 | 12.4 | 976 | 3 | US-09-195-868-14 | Sequence 14, Appl |
| 36 | 250 | 12.4 | 976 | 3 | US-09-418-540-2 | Sequence 2, Appli |
| 37 | 250 | 12.4 | 976 | 4 | US-09-969-528-2 | Sequence 2, Appli |
| 38 | 250 | 12.4 | 1187 | 3 | US-08-664-962B-8 | Sequence 8, Appli |
| 39 | 250 | 12.4 | 1187 | 3 | US-09-311-743-8 | Sequence 8, Appli |
| 40 | 250 | 12.4 | 1189 | 3 | US-09-195-868-15 | Sequence 15, Appl |
| 41 | 250 | 12.4 | 1229 | 3 | US-09-195-868-28 | Sequence 28, Appl |
| 42 | 220.5 | 10.9 | 398 | 3 | US-08-560-005-3 | Sequence 3, Appli |
| 43 | 220.5 | 10.9 | 398 | 3 | US-09-418-540-3 | Sequence 3, Appli |
| 44 | 220.5 | 10.9 | 398 | 4 | US-09-969-528-3 | Sequence 3, Appli |
| 45 | 180 | 8.9 | 230 | 4 | US-09-270-767-44142 | Sequence 44142, A |

ALIGNMENTS

RESULT 1

US-08-884-681-1

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; Sequence 1, Application US/08884681
; Patent No. 5955338
; GENERAL INFORMATION:
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Lal, Preeti
;   APPLICANT: Corley, Neil C.
;   APPLICANT: Shah, Purvi
;   TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Drive
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/884,681
;     FILING DATE: Filed Herewith
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Billings, Lucy J.
;     REGISTRATION NUMBER: 36,749
;     REFERENCE/DOCKET NUMBER: PF-0334 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-855-0555
;     TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 372 amino acids

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;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      IMMEDIATE SOURCE:
;      LIBRARY:  BRSTNOT03
;      CLONE:  638789
US-08-884-681-1
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Query Match          100.0%;  Score 2020;  DB 2;  Length 372;
Best Local Similarity 100.0%;  Pred. No. 1.3e-208;
Matches 372;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy     61 KLYGYVYSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
      |||
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Qy    121 IEDFGLHFVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
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Db    121 IEDFGLHFVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180

Qy    131 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
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Db    131 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240

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Db    241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY 300

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Db    361 REDPLGEAQPQI 372
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RESULT 2

US-09-258-643-1

; Sequence 1, Application US/09258643

; Patent No. 6277373

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Lal, Preeti

; APPLICANT: Corley, Neil C.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

Db 301 VSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL 360

Qy 361 REDPLGEAQPQI 372
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Db 361 REDPLGEAQPQI 372

RESULT 3

US-08-884-681-3

; Sequence 3, Application US/08884681

; Patent No. 5955338

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Lal, Preeti

; APPLICANT: Corley, Neil C.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/884,681

; FILING DATE: Filed Herewith

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0334 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 329 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 1399101

US-08-884-681-3

Query Match 88.7%; Score 1791; DB 2; Length 329;

Best Local Similarity 99.4%; Pred. No. 4.7e-184;

Matches 326; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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| Db | 2 | GLFGYWGNKGGVNICLKLYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPN | 61 |
| Qy | 105 | ILDHDLIIWFGDMNFRIEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGR | 164 |
| | | | |
| Db | 62 | ILDHDLIIWFGDMNFRIEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGR | 121 |
| Qy | 165 | LLFPPTYKFDRNSNDYDTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGY | 224 |
| | | | |
| Db | 122 | LLFPPTYKFDRNSNDYDTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGY | 181 |
| Qy | 225 | SSHMTYGISDHKPVSGTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPW | 284 |
| | | | |
| Db | 182 | SSHMTYGISDHKPVSGTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPW | 241 |
| Qy | 285 | DWIGLYKVGLRDVNDYVSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNSLR | 344 |
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| Db | 242 | DWIGLYKVGLRDVNDYVSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYRNSLR | 301 |
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RESULT 4

US-09-258-643-3

; Sequence 3; Application US/09258643

; Patent No. 6277373

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Lal, Preeti

; APPLICANT: Corley, Neil C.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/258,643

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/884,681

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0334 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 329 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 1399101
 US-09-258-643-3

Query Match 88.7%; Score 1791; DB 3; Length 329;
 Best Local Similarity 99.4%; Pred. No. 4.7e-184;
 Matches 326; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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| Qy | 45 | GLFGYWGNGGGVNICLKLYGYVSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDIPN | 104 |
| | | | |
| Db | 2 | GLFGYWGNGGGVNICLKLYGYVSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDIPN | 61 |
| Qy | 105 | ILDHDLIIWFGDMNFRIEDFGLHFVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGR | 164 |
| | | | |
| Db | 62 | ILDHDLIIWFGDMNFRIEDFGLHFVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGR | 121 |
| Qy | 165 | LLFPPTYKFDRNSNDYDTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGY | 224 |
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| | | | |
| Db | 182 | SSHMTYGISDHKPVSGTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPW | 241 |
| Qy | 285 | DWIGLYKVGLRDVNDYVSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLR | 344 |
| | | | |
| Db | 242 | DWIGLYKVGLRDVNDYVSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYRNSLR | 301 |
| Qy | 345 | SVVGISRPFQIPPGSLREDPLGEAQPQI | 372 |
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| Db | 302 | SVVGIRRPQIPPGSLREDPLGEAQPQI | 329 |

RESULT 5

US-08-884-681-4

; Sequence 4, Application US/08884681
 ; Patent No. 5955338
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,681
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0334 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1019103
US-08-884-681-4

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Query Match          21.4%; Score 432.5; DB 2; Length 942;
Best Local Similarity 37.0%; Pred. No. 4.6e-37;
Matches 90; Conservative 45; Mismatches 87; Indels 21; Gaps 4;

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Db      365 YAKVKLIRLVGIMLLLVVKQEHAAAYISEVEAETVGTGIMGRMGNKGGVAIRFQFHNTSIC 424

Qy      69 IINCHLPPHISNNYQRLEHF-DRILEMQNCE-GRDIP--NILDHDLIIWFGDMNFRIEDF 124
      ::| || || :| : : | || | : | :||: ||: ||: ||: ||:
Db      425 VVNSHLAAHIEEYERRNQDYKDICSRMQFCQPDPSLPPLTISNHDVILWLGLNYRIEEL 484

Qy      125 GLHFVRESIKNRCYGGGLWEKDQLSIAXKHDPDLLREFQEGRLLFPPTYKFDRNSNDYDTSE 184
      : |:: |: : : | : || | : | || | | ||||: | |:|: |||
Db      485 DVEKVKKLIEEKDFQMLYAYDQLKIQVAAKTVEGFTGEGELTFQPTYKYDTGSDDWDWTSE 544

Qy      185 KKRKPAWTDRIILWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSGTFDL 244
      | | ||| ||||: | ::: | || | ||||| ||:
Db      545 KCRAPAWCDRIILWKGGK-----NITQLSYQSHMALKTSDHKPVSSVFDI 587

Qy      245 ELK 247
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Db 588 GVR 590

RESULT 6

US-08-560-005-6

; Sequence 6, Application US/08560005

; Patent No. 6001354

; GENERAL INFORMATION:

; APPLICANT: Pot, David A.

; APPLICANT: Williams, Lewis T.

; APPLICANT: Jefferson, Anne Bennett

; APPLICANT: Majerus, Philip W.

; TITLE OF INVENTION: No. 6001354e1 Grb2 Associating Protein and Nucleic

; TITLE OF INVENTION: Acids Encoding Therefor

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/560,005

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Dow, Karen B.

; REGISTRATION NUMBER: 29,684

; REFERENCE/DOCKET NUMBER: 2307K-0624000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 942 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Region

; LOCATION: 1..942

; OTHER INFORMATION: /note= "majptase"

US-08-560-005-6

Query Match 21.4%; Score 432.5; DB 3; Length 942;

Best Local Similarity 37.0%; Pred. No. 4.6e-37;

Matches 90; Conservative 45; Mismatches 87; Indels 21; Gaps 4;

Qy 9 FIKVSHVRMQGILLVFAKYQHLPYIQILSTKSTPTGLFGYWGNKGGVNICKLYGYYS 68

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Db 365 YAKVKLIRLVGIMLLLYVKQEAAYISEVEAETVGTGIMGRMGNKGGVAIRFQFHNTSIC 424

Qy 69 IINCHLPPHISNNYQRLEHF-DRILEMQNCE-GRDIP--NILDHDLIIWFGDMNFRIEDF 124
 Db 425 VVNSHLAAHIEEYERRNQDYKDICSRMQFCQPDPSLPPLTISNHDVILWMGDLNYRIEEL 484

Qy 125 GLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLLPPTYKFDRNSNDYDTSE 184
 Db 485 DVEKVKKLIEEKDFQMLYAYDQLKIQVAAKTVEGFTTEGELTFQPTYKYDTGSDDWDTSE 544

Qy 185 KKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSGTFDL 244
 Db 545 KCRAPAWCDRILWKGK-----NITQLSYQSHMALKTSDHKPVSSVFDI 587

Qy 245 ELK 247
 Db 588 GVR 590

RESULT 7

US-09-258-643-4

; Sequence 4, Application US/09258643
 ; Patent No. 6277373
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/258,643
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/884,681
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0334 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 942 amino acids


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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1019103
US-09-258-643-4

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Query Match          21.4%; Score 432.5; DB 3; Length 942;
Best Local Similarity 37.0%; Pred. No. 4.6e-37;
Matches    90; Conservative    45; Mismatches    87; Indels    21; Gaps    4;

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Qy      9 FIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICLKLYGYVVS 68
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Db     365 YAKVKLIRLVGIMLLLYVKQEAAYISEVEAETVGTGIMGRMGNGGGVAIRFQFHNTSIC 424

Qy     69 IINCHLPPHISNNYQRLEHF-DRILEMQNCE-GRDIP--NILDHDLIIWFGDMNFRIEDF 124
      :|:| || || :| : : | || |: :| | :||:|:| ||:|:|:|:
Db     425 VVNSHLAAHIEEYERRNQDYKDICSRMQFCQPDPSLPPLTISNHDVILWLGLDLYRIEEI 484

Qy    125 GLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLLPPTYKFDRNSNDYDTSE 184
      : |:: |: : : |: ||| | : ||| | ||||:| |:|:|:|
Db    485 DVEKVKKLIEEKDFQMLYAYDQLKIQVAAKTVFEGFTEGELTFQPTYKYDTGSDDWDYDTSE 544

Qy    185 KKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSGTFDL 244
      | | ||| ||||:| ::: | ||| ||||| ||:
Db    545 KCRAPAWCDRILWKGK-----NITQLSYQSHMALKTSDHKPVSSVFDI 587

Qy    245 ELK 247
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Db    588 GVR 590

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RESULT 8

US-09-418-540-6

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; Sequence 6, Application US/09418540
; Patent No. 6296848

```

GENERAL INFORMATION:

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; APPLICANT: Pot, David A.
; APPLICANT: Williams, Lewis T.
; APPLICANT: Jefferson, Anne Bennett
; APPLICANT: Majerus, Philip W.
; TITLE OF INVENTION: No. 6296848el Grb2 Associating Protein and Nucleic
; TITLE OF INVENTION: Acids Encoding Therefor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

```

COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/418,540
; FILING DATE: 14-OCT-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/560,005
; FILING DATE: 17-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-0624000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..942
; OTHER INFORMATION: /note= "majptase"
US-09-418-540-6

```

```

Query Match          21.4%; Score 432.5; DB 3; Length 942;
Best Local Similarity 37.0%; Pred. No. 4.6e-37;
Matches 90; Conservative 45; Mismatches 87; Indels 21; Gaps 4;

```

```

Qy      9 FIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICLKLYGYVVS 68
      : || :|: ||: ||: | :| || : : ||: | ||||| | : : :
Db      365 YAKVKLIRLVGIMLLLYVKQEHAAYISEVEAETVGTGIMGRMGNGGGVAIRFQPHNTSIC 424

Qy      69 IINCHLPPHISNNYQRLEHF-DRILEMQNCE-GRDIP--NILDHDLIIWFGDMNFRIEDF 124
      ::| || || :| : : | || | :| | :||:|:| ||:|:| ||:
Db      425 VVNSHLAAHIEEYERRNQDYKDICSRMQFCQPDPSLPPLTISNHDVILWMGDLNRYIEEL 484

Qy      125 GLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLFPPTYKFDRNSNDYDTSE 184
      : |:: |: : : |: ||| | : || | | ||||:| |:|:| |||
Db      485 DVEKVKKLIEEKDFQMLYAYDQLKIQVAAKTVFEGFTEGELTFQPTYKYDTGSDDWDTSE 544

Qy      185 KKRKPAWTDRLWRLKRQPCAGPDTPIPPASH7SLSLRGYSSHMTYGISDHKPVSGTFDL 244
      | | ||| |||||: | ::: | ||| ||||| ||:
Db      545 KCRAPAWCDRILWKGK-----NITQLSYQSHMALKTSDHKPVSSVFDI 587

Qy      245 ELK 247
      ::
Db      588 GVR 590

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RESULT 9
US-09-969-528-6
; Sequence 6, Application US/09969528
; Patent No. 6472197
; GENERAL INFORMATION:
; APPLICANT: Pot, David A.

```

```

; Williams, Lewis T.
; Jefferson, Anne Bennett
; Majerus, Philip W.
; TITLE OF INVENTION: No. 6472197e1 Grb2 Associating Protein and Nucleic
; Acids Encoding Therefor
;
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/969,528
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/560,005
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-0624000
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..942
; OTHER INFORMATION: /note= "majptase"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-969-528-6

```

```

Query Match          21.4%; Score 432.5; DB 4; Length 942;
Best Local Similarity 37.0%; Pred. No. 4.6e-37;
Matches 90; Conservative 45; Mismatches 87; Indels 21; Gaps 4;

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```

Qy      9 FIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNKGGVNICKLYGYVVS 68
      : || :|: ||:|::| :| || : :: ||: | ||||| | : : :
Db     365 YAKVKLIRLVGIMLLLYVKQEHAAAYISEVEAETVGTGIMGRMGNGGGVAIRFQFHNTSIC 424

Qy     69 IINCHLPPHISNNYQRLEHF-DRILEMQNCE-GRDIP--NILDHDLIIWFGDMNFRIEDF 124
      ::| || || :| : : | || : : | :||:|:| ||:|:|::|
Db    425 VVNSHLAAHIEEYERRNQDYKDICSRMQFCQPDPSLPPLTISNHDVILWMGDLNRYRIEEL 484

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QY 125 GLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDYDTSE 184
 : |:: |: : : |: ||| | : | || | | |||:| |:|:||||
 Db 485 DVEKVKKLTIEEKDFQMLYAYDQLKIQVAAKTVFEGFTEGELTFQPTYKYDTGSDDWDTSE 544
 QY 185 KKRKPAWTDRILWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSGTFDL 244
 | | ||| ||||: | ::: | ||| ||||| ||:
 Db 545 KCRAPAWCDRILWK GK-----NITQLSYQSHMALKTSDHKPVSSVFDI 587
 QY 245 ELK 247
 ::
 Db 588 GVR 590

RESULT 10

US-08-560-005-7

; Sequence 7, Application US/08560005
 ; Patent No. 6001354
 ; GENERAL INFORMATION:
 ; APPLICANT: Pot, David A.
 ; APPLICANT: Williams, Lewis T.
 ; APPLICANT: Jefferson, Anne Bennett
 ; APPLICANT: Majerus, Philip W.
 ; TITLE OF INVENTION: No. 6001354e1 Grb2 Associating Protein and Nucleic
 ; TITLE OF INVENTION: Acids Encoding Therefor
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/560,005
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dow, Karen B.
 ; REGISTRATION NUMBER: 29,684
 ; REFERENCE/DOCKET NUMBER: 2307K-0624000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 968 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Region
 ; LOCATION: 1..968

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;      OTHER INFORMATION:  /note= "ocr1"
US-08-560-005-7
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Query Match 18.2%; Score 368.5; DB 3; Length 968;
Best Local Similarity 29.1%; Pred. No. 3.8e-30;
Matches 102; Conservative 55; Mismatches 121; Indels 73; Gaps 8;

| Qy | 5 | SPLSFIKVSHVRMQGILLLVFAKYQHLPIYQILSTKSTPTGLFGYWGNGKGVNICKLYG | 64 |
|----|-----|---|-----|
| Db | 382 | SKAKYKKVQLVRLVGMMLLIFARKDQCRYIRDIATETVGTGIMGKMGNKGGVAVRFVFHN | 441 |
| Qy | 65 | YYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDI-----PNILDHD | 109 |
| Db | 442 | TTFCIVNSHLAAHVED-----LERRNQDYKDICARMSFVVPNQTLPLQNLIMKHE | 490 |
| Qy | 110 | LIIWFGDMNFRIEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLFPP | 169 |
| Db | 491 | VVIWMGDLNRYRLCMPDANEVKS LINKDLQRL LKFDQLNIQRTQKKA FVDFNEGEIKFIP | 550 |
| Qy | 170 | TYKFDRNSNDYDTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMT | 229 |
| Db | 551 | TYKYDSKTD RWDSSGKCRVPAWCDRILWR-----GTNVNQLNYSRSHML | 593 |
| Qy | 230 | YGISDHKPVSGTFDLELKPL-----VSAPLIVLMPEDLWTVENDMMVSYS-STSDFPS | 281 |
| Db | 594 | LKTS DHKPV SALFHIGVKVVDERRYRKVFEDSVRIMDR---MENDFLPSLELSRREF-- | 647 |
| Qy | 282 | SPWDWIGLYKVGLRDVNDYVSYAWVGDSKVSCSDNLNQVYIDISNIPTTED | 332 |
| Db | 648 | -----VFENVKFRLOLQKGKFOISNN-GQVPCHFSFIPK LND | 682 |

RESULT 11.

US-09-413-540-7

; Sequence 7, Application US/09418540

; Patent No. 6296848

; GENERAL INFORMATION:

; APPLICANT: Pot, David A.

; APPLICANT: Williams, Lewis T.

APPLICANT: Jefferson, Anne Bennett

APPLICANT: Majerus, Philip W.

; TITLE OF INVENTION: No. 6296848e1 Grb2 Associating Protein and Nucleic

10 TITLE OF INVENTION: Acids Encoding Therefor

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

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; STATE: California
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; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
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;  COMPUTER:  IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS

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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:

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; Patent No. 6472197
; GENERAL INFORMATION:
;   APPLICANT: Pot, David A.
;               Williams, Lewis T.
;               Jefferson, Anne Bennett
;               Majerus, Philip W.
;   TITLE OF INVENTION: No. 6472197e1 Grb2 Associating Protein and Nucleic
;                       Acids Encoding Therefor
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Townsend and Townsend and Crew
;       STREET: One Market Plaza, Steuart Tower, Suite 2000
;       CITY: San Francisco
;       STATE: California
;       COUNTRY: USA
;       ZIP: 94105
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/969,528
;       FILING DATE: 01-Oct-2001
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/560,005
;       FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Dow, Karen B.
;       REGISTRATION NUMBER: 29,684
;       REFERENCE/DOCKET NUMBER: 2307K-0624000
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 415-326-2400
;       TELEFAX: 415-326-2422
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 968 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       FEATURE:
;           NAME/KEY: Region
;           LOCATION: 1..968
;           OTHER INFORMATION: /note= "ocr1"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-969-528-7

```

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Query Match          18.2%; Score 368.5; DB 4; Length 968;
Best Local Similarity 29.1%; Pred. No. 3.8e-30;
Matches 102; Conservative 55; Mismatches 121; Indels 73; Gaps 8;

```

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Qy      5 SPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNKGGVNICKLYG 64
|      : || ||: |::||:|: |:: ::|: |:: | ||||| : :
Db      382 SKAKYKKVQLVRLVGMMLLIFARKDQCRYIARDIATETVGTGIMGKMGNGGGVAVRFVFN 441
Qy      65 YYVSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDI-----PNILDHD 109

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| | | | |
|----|-----|---|-----|
| Db | 442 | TTFCIVNSHLAAHVED-----LERRNQDYKDICARMSFVVPNQTLPLQNLNIMKHE | 490 |
| Qy | 110 | LIWFGDMNFRIEDFGLHFVRESIKNRCYGGWLEKDQLSIAKKHDPDLLREFQEGRLFP | 169 |
| Db | 491 | VVIWMGDLNRYRLCMPDANEVKSINKKDLQRLKFDQLNIQRTQKKAQVDFNEGEIKFIP | 550 |
| Qy | 170 | TYKFDRNSNDYDTSEKKRKPATDRILWRLKRPCAGPDTPIPPASHFSLSLRGYSSHMT | 229 |
| Db | 551 | TYKYDSKTDWRDSSGKCRVPAWCDRILWR-----GTNVNQLNRYSHML | 593 |
| Qy | 230 | YGISDHKPVSGTFDLELKPL-----VSAPLIVLMPEDLWTVENDMMVSY-STSDFPS | 281 |
| Db | 594 | LKTSDHKPVSAFLHIGVKVVDERRYKVFEDSVRIMDR---MENDFLPSLELSRREF-- | 647 |
| Qy | 282 | SPWDWIGLYKVGLRDVNDYVSYAWVGDSKVSCSDNLNQVYIDISNIPTTED | 332 |
| Db | 648 | -----VFENVKFRQLQKGKQFQISNN-GQVPCFHSFIPKLND | 682 |

RESULT 13

US-08-884-681-5

; Sequence 5, Application US/08884681

; Patent No. 5955338

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Lal, Preeti

; APPLICANT: Corley, Neil C.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/884,681

; FILING DATE: Filed Herewith

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0334 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 5:


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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 901 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: GenBank
;   CLONE: 1420920
US-08-884-681-5
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Query Match          18.2%; Score 367.5; DB 2; Length 901;
Best Local Similarity 29.4%; Pred. No. 4.3e-30;
Matches 100; Conservative 58; Mismatches 131; Indels 51; Gaps 8;
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Qy      5 SPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGKGGVNICKLYG 64
      | : || ||: |:|:|:|: | |: :|:|: ||: | ||||| : :
Db    307 SKAKYKKVQLVRLVGMMLLIFARKDQCRYIIRDIATETVGTGIMGKMGNGKGGVAVRFVFNH 366

Qy     65 YYVSIINCHLPPHISNNYQRLEHFDRIEMQN--CEGRDIP--NILDHDLIIWFGDMNFR 120
      |:| || |: : :| : : | : : :| ||: |:|:| ||:|:|
Db    367 TTFCIVNSHLAAHVEDFERNQDYKDICARMSFVVPNQTLPLNIMKHEVVIWLGDLNRYR 426

Qy    121 IEDFGLHFVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGRLFPPTYKFDRNSNDY 180
      : : |: | : : |||:| : :| || : | |||:| : : :
Db    427 LCMPDANEVKSLINKKDLQRLKFDQLNIQRTQKKAQVDFNEGEIKFIPTYKYDSKTDWR 486

Qy    181 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
      |:| | | ||| ||||| : : | ||| |||||
Db    487 DSSGKCRVPAWCDRLWR-----GTNVNQLNRYRSHMELKTSDHKPVSA 529

Qy    241 TFDLELKPL-----VSAPLIVLMPEDLWTVENDMMVSYS-STSDFPSSPWDWIGLYKV 292
      | : :| : | : :| :| : | :|
Db    530 LFHIGVKVVDERRYRKVFEDSVRIMDR---MENDFLPSLELSRREF----- 572

Qy    293 GLRDVNDYVSYAWVGDSKVSCSDNLNQVYIDISNIPTTED 332
      | : | : : | |:| || | || |
Db    573 ----VFENVKFRQLQKGKQISNN-GQVPCHFSFIPKLND 607
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RESULT 14

US-09-258-643-5

; Sequence 5, Application US/09258643

; Patent No. 6277373

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Lal, Preeti

; APPLICANT: Corley, Neil C.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

RESULT 15

US-09-949-016-7283

; Sequence 7283, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7283

; LENGTH: 952

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-7283

Query Match 18.2%; Score 367.5; DB 4; Length 952;
Best Local Similarity 29.4%; Pred. No. 4.7e-30;
Matches 100; Conservative 58; Mismatches 131; Indels 51; Gaps 8;

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Qy      5 SPLSFIKVSVMQGIALLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGKGGVNICKLYG 64
      | : || ||: |::||:|:: |:: ::|:: ||: | ||||| : :
Db      366 SKAKYKKVQLVRLVGMMLLIFARKDQCRYIRDIAETETVGTGIMGKMGNGKGGVAVRFVFN 425
Qy      65 YYVSIINCHLPPHISNNYQRLEHFDRIEMQN--CEGRDIP--NILDHDLIIWFGDMNFR 120
      |:| || |: : :| : : | : : :| ||: |::|| ||:|:|
Db      426 TTFCIVNSHLAAHVEDFERNQDYKDICARMSFVVPNQTLPLQNLNIMKHEVVIWLGDLN 485
Qy      121 IEDFGLHFVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
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Db      436 LCPDANEVKS LINKKDLQRLKFDQLNIQRTQKKA FVDFNEGEIKFIPTYKYDSKTDRW 545
Qy      181 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
      |:| || ||| ||||| ::: | ||| |||||
Db      546 DSSGKCRVPAWCDRIIWR-----GTNVNQLNYSRSHMELKTS DHKPVSA 588
Qy      241 TFDLELKPL-----VSAPLIVLMPEDLWTVENDMMVSYS-STSDFPSSPWDWIGLYKV 292
      | : :| : : :| : :| :| :| :| :|
Db      589 LFHIGVKVVDERRYRKVFEDSVRIMDR----MENDFLPSLELSRREF----- 631
Qy      293 GLRDVNDYVSYAWVGDSKVS CSDNLNQVYIDISNIPTTED 332
      | : | : : | |:| || ||| |
Db      632 ----VFENVKFRQLQKEKFQISNN-GQVPCHFSFIPKLND 666

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Search completed: February 10, 2005, 18:03:02

Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 17:50:47 ; Search time 133 Seconds
(without alignments)
913.915 Million cell updates/sec

Title: US-09-892-287-1
Perfect score: 2020
Sequence: 1 MDVLSPLSFIKVSVMQGI.....FQIPPGSLREDPLGEAQPQI 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | | |
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| 1 | 2020 | 100.0 | 372 | 9 | US-09-892-287-1 | Sequence 1, Appli | |
| 2 | 2020 | 100.0 | 448 | 13 | US-10-161-510-14 | Sequence 14, Appl | |
| 3 | 2012 | 99.6 | 478 | 13 | US-10-161-510-11 | Sequence 11, Appl | |
| 4 | 2010 | 99.5 | 372 | 13 | US-10-161-510-13 | Sequence 13, Appl | |
| 5 | 2010 | 99.5 | 448 | 13 | US-10-161-510-12 | Sequence 12, Appl | |
| 6 | 1791 | 88.7 | 329 | 9 | US-09-892-287-3 | Sequence 3, Appli | |
| 7 | 872.5 | 43.2 | 1001 | 15 | US-10-415-147-3 | Sequence 3, Appli | |
| 8 | 868.5 | 43.0 | 639 | 15 | US-10-104-047-3268 | Sequence 3268, Ap | |
| 9 | 868.5 | 43.0 | 639 | 15 | US-10-108-260A-3425 | Sequence 3425, Ap | |
| 10 | 868.5 | 43.0 | 1006 | 15 | US-10-114-270-84 | Sequence 84, Appl | |
| 11 | 868.5 | 43.0 | 1006 | 15 | US-10-415-147-12 | Sequence 12, Appl | |
| 12 | 831.5 | 41.2 | 751 | 15 | US-10-415-147-2 | Sequence 2, Appli | |
| 13 | 831.5 | 41.2 | 1056 | 13 | US-10-161-510-10 | Sequence 10, Appl | |
| 14 | 683.5 | 33.8 | 279 | 14 | US-10-106-698-4755 | Sequence 4755, Ap | |
| 15 | 541.5 | 26.8 | 162 | 15 | US-10-264-049-4157 | Sequence 4157, Ap | |
| 16 | 500.5 | 24.8 | 397 | 16 | US-10-408-765A-211 | Sequence 211, App | |
| 17 | 460.5 | 22.8 | 357 | 9 | US-09-740-046-8 | Sequence 8, Appli | |
| 18 | 432.5 | 21.4 | 942 | 9 | US-09-892-287-4 | Sequence 4, Appli | |
| 19 | 432.5 | 21.4 | 942 | 9 | US-09-969-528-6 | Sequence 6, Appli | |
| 20 | 368.5 | 18.2 | 968 | 9 | US-09-969-528-7 | Sequence 7, Appli | |
| 21 | 367.5 | 18.2 | 901 | 9 | US-09-892-287-5 | Sequence 5, Appli | |
| 22 | 367.5 | 18.2 | 968 | 16 | US-10-408-765A-1484 | Sequence 1484, Ap | |
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| 24 | 327.5 | 16.2 | 1443 | 16 | US-10-408-765A-1098 | Sequence 1098, Ap | |
| 25 | 327.5 | 16.2 | 1496 | 16 | US-10-755-889-672 | Sequence 672, App | |
| 26 | 327.5 | 16.2 | 1510 | 15 | US-10-381-333-12 | Sequence 12, Appl | |
| 27 | 320.5 | 15.9 | 1166 | 16 | US-10-437-963-159124 | Sequence 159124, | |
| 28 | 318 | 15.7 | 657 | 16 | US-10-437-963-144470 | Sequence 144470, | |
| 29 | 316.5 | 15.7 | 1114 | 9 | US-09-740-046-10 | Sequence 10, Appl | |
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| 31 | 303.5 | 15.0 | 513 | 15 | US-10-424-599-147057 | Sequence 147057, | |
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| 35 | 290.5 | 14.4 | 946 | 9 | US-09-969-528-4 | Sequence 4, Appli | |
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| 38 | 290 | 14.4 | 536 | 15 | US-10-425-114-63809 | Sequence 63809, A | |
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| 44 | 280.5 | 13.9 | 566 | 16 | US-10-437-963-166113 | Sequence 166113, | |
| 45 | 280.5 | 13.9 | 600 | 15 | US-10-425-114-63760 | Sequence 63760, A | |

ALIGNMENTS

RESULT 1

US-09-892-287-1

; Sequence 1, Application US/09892287

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; Patent No. US20020127217A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Lal, Preeti
; Corley, Neil C.
; Shah, Purvi
; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL
; (4,5) BISPHOSPHATE 5-PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,287
; FILING DATE: 26-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/258,643
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0334 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT03
; CLONE: 638789
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-392-287-1

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Query Match          100.0%; Score 2020; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.2e-188;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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US-10-161-510-14
; Sequence 14, Application US/10161510
; Publication No. US20020192695A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: PIBs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-074C
; CURRENT APPLICATION NUMBER: US/10/161,510
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-510-14

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Query Match          100.0%; Score 2020; DB 13; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.8e-188;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-10-161-510-11

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; Sequence 11, Application US/10161510
; Publication No. US20020192695A1
; GENERAL INFORMATION:
;   APPLICANT: EXELIXIS, INC.
;   TITLE OF INVENTION: PIBs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
;   FILE REFERENCE: EX02-074C
;   CURRENT APPLICATION NUMBER: US/10/161,510
;   CURRENT FILING DATE: 2002-06-03
;   PRIOR APPLICATION NUMBER: US 60/296,076
;   PRIOR FILING DATE: 2001-06-05
;   PRIOR APPLICATION NUMBER: US 60/328,605
;   PRIOR FILING DATE: 2001-10-10
;   PRIOR APPLICATION NUMBER: US 60/357,253
;   PRIOR FILING DATE: 2002-02-15
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 478
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (56)..(56)
;   OTHER INFORMATION: "X" is any amino acid
US-10-161-510-11

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Query Match          99.6%;  Score 2012;  DB 13;  Length 478;
Best Local Similarity 99.7%;  Pred. No. 1.9e-187;
Matches 371;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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| Db | 167 | KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 226 |
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| Qy | 181 | DTSEKKRKPAWTDRILWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 240 |
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| Db | 287 | DTSEKKRKPAWTDRILWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG | 346 |
| Qy | 241 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY | 300 |
| | | | |
| Db | 347 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY | 406 |
| Qy | 301 | VSIAWVGDSKVSCLNQLNQVYIDISNIPTTEDEFLLCYYSNLSRSVVGISRPFIIPGSL | 360 |
| | | | |
| Db | 407 | VSIAWVGDSKVSCLNQLNQVYIDISNIPTTEDEFLLCYYSNLSRSVVGISRPFIIPGSL | 466 |
| Qy | 361 | REDPLGEAQPQI | 372 |
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RESULT 4

US-10-161-510-13

; Sequence 13, Application US/10161510

; Publication No. US20020192695A1

; GENERAL INFORMATION:

; APPLICANT: EXELIXIS, INC.

; TITLE OF INVENTION: PIBs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

; FILE REFERENCE: EX02-074C

; CURRENT APPLICATION NUMBER: US/10/161,510

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US 60/296,076

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/328,605

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/357,253

; PRIOR FILING DATE: 2002-02-15

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn, version 3.1

; SEQ ID NO 13

; LENGTH: 372

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-161-510-13

Query Match 99.5%; Score 2010; DB 13; Length 372;
 Best Local Similarity 99.5%; Pred. No. 2.1e-187;
 Matches 370; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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| Qy | 241 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY | 300 |
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| Db | 241 | TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY | 300 |
| Qy | 301 | VSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL | 360 |
| | | | |
| Db | 301 | VSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQIPPGSL | 360 |
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| Db | 361 | REDPLGEAQPQI | 372 |

RESULT 5

US-10-161-510-12
; Sequence 12, Application US/10161510
; Publication No. US20020192695A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: PIBs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-074C
; CURRENT APPLICATION NUMBER: US/10/161,510
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-510-12

Query Match 99.5%; Score 2010; DB 13; Length 448;
Best Local Similarity 99.5%; Pred. No. 2.7e-187;
Matches 370; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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| | | | |
| Db | 77 | MDVLSPLSFIKVS HVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL | 136 |

Qy 61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
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 Db 137 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 196

Qy 121 IEDFGLHFVRESIKNRCYGGLWEKDQLSIAKKHDPLLREFQEGRLLFPPTYKFDRNSNDY 180
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 Db 197 IEDFGLHFVRESIKNRCYGGLWEKDQLSIAKKHDPLLREFQEGRLLFPPTYKFDRNSNDY 256

Qy 181 DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
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Qy 241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
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 Db 317 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVNDY 376

Qy 301 VSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNLSRSVVGISRPFIIPPGSL 360
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 Db 437 REDPLGEAQPQI 448

RESULT 6

US-09-892-287-3

; Sequence 3, Application US/09892287

; Patent No. US20020127217A1

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; Lal, Preeti

; Corley, Neil C.

; Shah, Purvi

; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL

; (4,5) BISPHOSPHATE 5-PHOSPHATASE

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/892,287

; FILING DATE: 26-Jun-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/258,643

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0334 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 329 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 1399101
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-892-287-3

Query Match 88.7%; Score 1791; DB 9; Length 329;
 Best Local Similarity 99.4%; Pred. No. 4.3e-166;
 Matches 326; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 45 | GLFGYWGNGGGVNICLKLYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPN | 104 |
| | | | |
| Db | 2 | GLFGYWGNGGGVNICLKLYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPN | 61 |
| Qy | 105 | ILDHDLIIWFGDMNFRIEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGR | 164 |
| | | | |
| Db | 62 | ILDHDLIIWFGDMNFRIEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGR | 121 |
| Qy | 165 | LLFPPTYKFDRNSNDYDTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGY | 224 |
| | | | |
| Db | 122 | LLFPPTYKFDRNSNDYDTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGY | 181 |
| Qy | 225 | SSHMTYGISDHKPVSGTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPW | 284 |
| | | | |
| Db | 182 | SSHMTYGISDHKPVSGTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPW | 241 |
| Qy | 285 | DWIGLYKVGLRDVNDYVSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLR | 344 |
| | | | |
| Db | 242 | DWIGLYKVGLRDVNDYVSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYRNSLR | 301 |
| Qy | 345 | SVVGISRPFQIPPGSLREDPLGEAQPQI | 372 |
| | | | |
| Db | 302 | SVVGIRRPFQIPPGSLREDPLGEAQPQI | 329 |

RESULT 7

US-10-415-147-3

; Sequence 3, Application US/10415147
 ; Publication No. US20040043399A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer AG
 ; TITLE OF INVENTION: REGULATION OF HUMAN INOSITOL POLYPHOSPHATE 5-PHOSPHATASE
 ; FILE REFERENCE: LIO235Foreign Countries
 ; CURRENT APPLICATION NUMBER: US/10/415,147
 ; CURRENT FILING DATE: 2003-04-25

```

; PRIOR APPLICATION NUMBER: US 60/243,745
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 60/257,302
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 60/314,660
; PRIOR FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1001
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-415-147-3

```

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Query Match          43.2%; Score 372.5; DB 15; Length 1001;
Best Local Similarity 47.5%; Pred. No. 1.1e-75;
Matches 169; Conservative 56; Mismatches 126; Indels 5; Gaps 4;

```

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QY      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGKGGVNICL 60
      || | | :| : || |||||::||:|||| ||::: : | | ||| |||||::: |
Db      483 MDALGPFNFVLVSTVRMQGVILLVFAKYHLPFLRDVQTDCTRTGLGGYWGNGKGGVSVRL 542

QY      61 KLYGYVYSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
      :| : : :||| | | : || :| || :| :| |||||: |||: |||
Db      543 AAFGHMLCFLNCHLPAHMDKAEQRKDNFQTILSLQQFQGPAGHGILDHDLVFWFGDLNFR 602

QY      121 IEDFGLHFVRESIKNRCYGGWLWEKDQLSIAKKHDPDLLREFQEGRLLPPTYKFDRNSNDY 180
      || : ||||: :| : |||||::|| |::: |||| | | ||: ||| :| |
Db      603 IESYDLHFVKFAIDSNQLHQLWEKDQLNMAKNTWPILKGFQEGPLNFAPTFKFQVGTNKY 662

QY      181 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPV 239
      ||| ||||| |||||::: | | || :| || :| :| ||| | :||| | :
Db      663 DTSAKRKPAWTDRLWKVK-APSGGP-SPSGRESHRLQVTQHSYRSHMEYTVSDHKPVA 720

QY      240 GTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVND 299
      | | : ||: | | | :| | : | | |||||: || | | |
Db      721 ARFLLQFAFRDDVPLVRLEVADEWARPEQAVVRYRVETVFARSSWDWIGLYRVGFRHCKD 780

QY      300 YVSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQI 355
      ||: | | :| | : || :| :| :| | | : :| :| :| |
Db      781 YVAYVWAKHEEV--DGNIIQVTFSEESLPKGHGDFILGYSSHHSILIGVTEPFQI 834

```

RESULT 8

US-10-104-047-3268

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; Sequence 3268, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1

```

; SEQ ID NO 3268
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3268

Query Match 43.0%; Score 868.5; DB 15; Length 639;
Best Local Similarity 47.8%; Pred. No. 1.4e-75;
Matches 170; Conservative 54; Mismatches 127; Indels 5; Gaps 4;

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Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGKGGVNICL 60
      || | | :|: || |||||::||:|||| ||::: : | | || | |||||::: |
Db     121 MDALGPFNFVLVSSVRMQGVILLLVFAKYHLPFLRDVQTDCTRTGLGGYWGNGKGGVSVRL 180

Qy     61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
      :|: : : ||||| | : || :| || :| :| |||||: ||||:||||
Db    181 AAFGHMLCFLNCHLPAHMDKAEQRKDNFQTILSLQQFQGPQAQGILDHDLVFWFGDLNFR 240

Qy    121 IEDFGLHFVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
      || : ||||: :| : |||||::|| |:: |||| | | ||:|||| :| |
Db    241 IESYDLHFVKFAIDSDQLHQLWEKDQLNMAKNTWPILKGFQEGPLNFAPTFKFDVGTNKY 300

Qy    181 DTSEKKRKPATDRILWRLKRQPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPVS 239
      ||| ||||| |||||:::| | || :| || :| ||| | :|||:::
Db    301 DTSAKKRKPATDRILWKVK-APGGGP-SPSGRKSHRLQVTQHSYRSHMEYTVSDHKPVA 358

Qy    240 GTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVND 299
      | | : ||: | | | :| | : | | |||||: || | |
Db    359 AQFLLQFAFRDDMPLVRLEVADEWVRPEQAVVPYRMETVFARSSWDWIGLYRVGFRHCKD 418

Qy    300 YVSYAWVGDSKVSCSDNLNQYVIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFI 355
      ||:| | | | | || :| :|: ||||: :||: |||
Db    419 YVAYVWAKHEDV--DGNTYQVTFSEESLPKGHGDFILGYYSNHSILIGITEPFI 472
```

RESULT 9

US-10-108-260A-3425

; Sequence 3425, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3425
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3425

Query Match 43.0%; Score 868.5; DB 15; Length 639;
Best Local Similarity 47.8%; Pred. No. 1.4e-75;
Matches 170; Conservative 54; Mismatches 127; Indels 5; Gaps 4;


```

; APPLICANT: Stone, David J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Rothenberg, Mark E.
; TITLE OF INVENTION: No. US20040030110A1e1 Proteins and Nucleic Acids Encoding
Same
; FILE REFERENCE: 21402-322C
; CURRENT APPLICATION NUMBER: US/10/114,270
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/281,086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 84
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-270-84

```

| | | | |
|----|-----|--|-----|
| Qy | 1 | MDVLSPLSFYIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNKGGVNICL | 60 |
| | | : : : : : : : : : : | |
| Db | 488 | MDALGPFNFVLVSSVRMQGVILLLLFAKYIHLPLFLRDVQTDCTRTGLGGYWGNKGGVSVRL | 547 |
| Qy | 61 | KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 120 |
| | | : : : : : : : : : : : | |
| Db | 548 | AAFQHMLCFLNCHLPAHMDKAEQQRKDNFQTILSLQFQGPQAQGILDHDLVFWFGDLNFR | 607 |
| Qy | 121 | IEDFGLHFVRESIKNRCYGGWLWEKDQLSIAKKHDPDLLREFQEGRLLPPTYKFDRNSNDY | 180 |
| | | : : : : : : : : : : | |
| Db | 608 | IESYDLHFVKFAIDSDQLHLQWEKDQLNMAKNTWPILKGFQEGPLNFAPTFFKFDVGTNKY | 667 |
| Qy | 181 | DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPVS | 239 |
| | | : : : : : : : | |
| Db | 668 | DTSAKKRKPAWTDRIWLKVK-APGGGP-SPSGRKSHRLQVTQHSHYRSHMEYTVSDHKPVA | 725 |
| Qy | 240 | GTFDLELKLPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVND | 299 |


```

      | | :      | | : | | |      : | | : | | | | | | | : | | | |
Db      726 AQFLLQFAFRDDMPLVRLEVADEWVRPEQAVVRYRMETV FARSSWDWIGLYRVGFRHCKD 785

Qy      300 YVSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFI 355
      | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      786 YVAYVWAKHEDV--DGNTYQVTFSEESLPKGHGD FILGYYSNHSILIGITEPFQI 839

```

RESULT 11

US-10-415-147-12

; Sequence 12, Application US/10415147

; Publication No. US20040043399A1

; GENERAL INFORMATION:

; APPLICANT: Bayer AG

; TITLE OF INVENTION: REGULATION OF HUMAN INOSITOL POLYPHOSPHATE 5-PHOSPHATASE

; FILE REFERENCE: LIO235Foreign Countries

; CURRENT APPLICATION NUMBER: US/10/415,147

; CURRENT FILING DATE: 2003-04-25

; PRIOR APPLICATION NUMBER: US 60/243,745

; PRIOR FILING DATE: 2000-10-30

; PRIOR APPLICATION NUMBER: US 60/257,302

; PRIOR FILING DATE: 2000-12-26

; PRIOR APPLICATION NUMBER: US 60/314,660

; PRIOR FILING DATE: 2001-08-27

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 12

; LENGTH: 1006

; TYPE: PR1

; ORGANISM: Homo sapiens

US-10-415-147-12

Query Match 43.0%; Score 868.5; DB 15; Length 1006;

Best Local Similarity 47.8%; Pred. No. 2.7e-75;

Matches 170; Conservative 54; Mismatches 127; Indels 5; Gaps 4;

```

Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 60
      | | | | : | | | | | | | | | | | | | | | | | | | | | | |
Db      488 MDALGPFNFVLVSSVRMQGVILLVFAKYHLPFLRDVQTDCTRTGLGGYWGNGGGVSVRL 547

Qy      61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
      : | : : : | | | | | | : | | : | | | : | | | | | | | | | |
Db      548 AAFGHMLCFLNCHLPAHMDKAEQRKDNFQTILSLQQFGPGAQGILDHDLVFWFGDLNFR 607

Qy      121 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
      | | : | | | | : | : | | | | | | | | | | | | | | | | | | |
Db      608 IESYDLHFVKFAIDSDQLHQLWEKDQLNMAKNTWPILKGFQEGPLNFAPTFKFDVGTNKY 667

Qy      181 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPVS 239
      | | | | | | | | | | | | | | | | : | | | : | | : | | | | : | | | |
Db      668 DTSAKRKPAWTDRIWLKVK-APGGGP-SPSGRKSHRLQVTQHSYRSHMEYTVSDHKPVA 725

Qy      240 GTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRDVND 299
      | | :      | | : | | |      : | | : | | | | | | | | | | |
Db      726 AQFLLQFAFRDDMPLVRLEVADEWVRPEQAVVRYRMETV FARSSWDWIGLYRVGFRHCKD 785

Qy      300 YVSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFI 355

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RESULT 15

US-10-264-049-4157

```
; Sequence 4157, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4157
;   LENGTH: 162
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (120)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
acids
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (130)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
acids
US-10-264-049-4157
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Query Match          26.8%; Score 541.5; DB 15; Length 162;
Best Local Similarity 74.6%; Pred. No. 1.7e-44;
Matches 106; Conservative 0; Mismatches 7; Indels 29; Gaps 2;
```

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Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGKGGVNICL 60
      |||
Db      26 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGKGGVNICL 85

Qy      61 KLYGYYVSIINCHLPPHISN-----NYQRLEHFDRILEMQNCEGRDIPNII 106
      |||
Db      86 KLYGYYVSIINCHLPPHISTITSGWSTLTGSWRCXIVRARH-----PNIX 130

Qy      107 DHDLIWF GDMNFRIEDFGLHF 128
      |||
Db      131 DHDLIWF GDMNFRIEDFGLHF 152
```

Search completed: February 10, 2005, 18:05:21
Job time : 135 secs

OM protein - protein search, using sw model

Run on: February 10, 2005, 17:06:26 ; Search time 41 Seconds
(without alignments)
872.991 Million cell updates/sec

Title: US-09-892-287-1
Perfect score: 2020
Sequence: 1 MDVLSPLSFIKVSHVRMQGI.....FQIPPGSLREDPLGEAQPQI 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | | |
|--------|-------|-------|-------|--------|--------|----|--------------------|
| No. | Score | Query | Match | Length | DB | ID | Description |
| 1 | 406.5 | 20.1 | 1017 | 2 | T42384 | | inositol-1,4,5-tri |
| 2 | 367.5 | 18.2 | 893 | 2 | G59431 | | phosphatidylinosit |
| 3 | 367.5 | 18.2 | 970 | 2 | S29069 | | inositol polyphosp |
| 4 | 334 | 16.5 | 672 | 2 | A41075 | | inositol-1,4,5-tri |
| 5 | 334 | 16.5 | 1216 | 2 | JW0105 | | synaptojanin 2 alp |
| 6 | 328 | 16.2 | 1575 | 2 | S68448 | | synaptojanin, 170K |
| 7 | 300.5 | 15.3 | 1136 | 2 | D86190 | | hypothetical prote |
| 8 | 306 | 15.1 | 1305 | 2 | T00670 | | probable inositol |
| 9 | 300.5 | 14.9 | 753 | 2 | T19338 | | hypothetical prote |
| 10 | 298.5 | 14.8 | 331 | 2 | D96515 | | hypothetical prote |
| 11 | 297.5 | 14.7 | 401 | 2 | G84792 | | hypothetical prote |
| 12 | 291.5 | 14.4 | 1107 | 2 | S61667 | | probable membrane |
| 13 | 289.5 | 14.3 | 946 | 2 | S48433 | | inositol-1,4,5-tri |
| 14 | 284 | 14.1 | 1144 | 2 | F84725 | | probable inositol |
| 15 | 284 | 14.1 | 1258 | 2 | JC5765 | | inositol polyphosp |
| 16 | 279.5 | 13.8 | 1076 | 2 | T40141 | | phosphatidylinosit |
| 17 | 279 | 13.8 | 501 | 2 | H84727 | | probable inositol |
| 18 | 278.5 | 13.8 | 590 | 2 | C86465 | | probable inositol |

| | | | | | | |
|----|-------|------|------|---|--------|--------------------|
| 19 | 278 | 13.8 | 1183 | 2 | T39233 | probable Inositol |
| 20 | 277.5 | 13.7 | 574 | 2 | T48113 | inositol-1,4,5-tri |
| 21 | 276 | 13.7 | 889 | 2 | T40557 | probable inositol |
| 22 | 268.5 | 13.3 | 427 | 2 | C88883 | protein JC8.10 [im |
| 23 | 265.5 | 13.1 | 417 | 2 | E84430 | probable inositol |
| 24 | 265 | 13.1 | 1183 | 2 | S63046 | probable membrane |
| 25 | 264 | 13.1 | 613 | 2 | T51938 | inositol-1,4,5-tri |
| 26 | 264 | 13.1 | 670 | 2 | D96739 | hypothetical prote |
| 27 | 263 | 13.0 | 595 | 2 | T05087 | hypothetical prote |
| 28 | 260 | 12.9 | 646 | 2 | T51937 | probable inositol- |
| 29 | 251 | 12.4 | 1189 | 2 | JC6118 | SH2-containing ino |
| 30 | 250 | 12.4 | 1188 | 2 | JC4889 | phosphatidylinosit |
| 31 | 240 | 11.9 | 993 | 2 | G96680 | F5I14.11 [imported |
| 32 | 227.5 | 11.3 | 398 | 2 | S44627 | C50C3.7 protein - |
| 33 | 218 | 10.8 | 342 | 2 | T19021 | probable inositol |
| 34 | 172.5 | 8.5 | 384 | 2 | S66758 | probable membrane |
| 35 | 142.5 | 7.1 | 396 | 2 | T15465 | hypothetical prote |
| 36 | 114 | 5.6 | 743 | 2 | S19437 | hypothetical prote |
| 37 | 104.5 | 5.2 | 412 | 2 | S45721 | inositol-1,4,5-tri |
| 38 | 104.5 | 5.2 | 446 | 2 | A56733 | nuclear domain 10 |
| 39 | 102.5 | 5.1 | 412 | 2 | S44357 | inositol 1,4,5-tri |
| 40 | 99 | 4.9 | 1364 | 2 | T40839 | hypothetical prote |
| 41 | 98 | 4.9 | 384 | 2 | S76402 | hypothetical prote |
| 42 | 97.5 | 4.8 | 363 | 2 | A54167 | inositol-polyphosp |
| 43 | 95.5 | 4.7 | 954 | 2 | S46105 | glucan 1,4-alpha-g |
| 44 | 94.5 | 4.7 | 371 | 2 | AE1294 | hypothetical prote |
| 45 | 93 | 4.6 | 381 | 2 | T28378 | ORF MSV217 SCG gen |

ALIGNMENTS

RESULT 1

T42384

inositol-1,4,5-trisphosphate 5-phosphatase (EC 3.1.3.56) II, isoform 115K, membrane-associated - mouse

N;Alternate names: inositol trisphosphate phosphomonoesterase

C;Species: Mus musculus (house mouse)

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T42384

R;Matzaris, M.; O'Malley, C.; Badger, A.; Speed, C.; Bird, P.I.; Mitchell, C.A. submitted to the EMBL Data Library, December 1997

A;Description: Distinct membrane and cytosolic forms of inositol polyphosphate 5-phosphatase II. Efficient membrane localization requires two discrete domains.

A;Reference number: Z22143

A;Accession: T42384

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1017 <MAT>

A;Cross-references: UNIPROT:O54996; EMBL:AF040094; NID:g2766528; PID:g2766529; PIDN:AAB95412.1

A;Experimental source: brain

C;Genetics:

A;Gene: INPP5P

C;Keywords: phosphoric monoester hydrolase

Query Match

20.1%; Score 406.5; DB 2; Length 1017;

Best Local Similarity 34.1%; Pred. No. 1.7e-26;
Matches 86; Conservative 42; Mismatches 89; Indels 35; Gaps 4;

```

Qy      9 FIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFG----YWGNKGGVNICLKLYG 64
      : || ||: ||: ||: | :| || : :: || | ||||| | :|:
Db      415 YAKVKFVRLVGIMLLLYVKQEHAAYISEVEAETVGTGFMGRMSFQQGNKGGVAIRFQLHN 474

Qy      65 YYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIP-----NILDHDLIIWFG 115
      : ::| || | :| : : | | | | | ||: ||: |
Db      475 TSICVNVSHLAAHTEEYERRNQDYRDI-----CSRMQFPQVDPSQPPLTINKHDVILWLG 529

Qy     116 DMNFRIEDFGLHFVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDR 175
      |:|: |||: : |:: :: : : |: ||| | : | || : | |||: |
Db     530 DLNYRIEELDVGKVKKLVEEKAFQTLYAHDQLKIQVAARTIFDGFTEGEITFQPTYKYDT 589

Qy     176 NSNDYDTSEKKRKPAWTDRLWLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDH 235
      |:|: |||| | ||| ||||: | :: | ||| |||
Db     590 GSDDWDTSESARAPAWCDRILWKGK-----NITQLSYQSHMALKTSDH 632

Qy     236 KPVSGTFDLELK 247
      |||| ||: ::
Db     633 KPVSSVFDIGVR 644

```

RESULT 2

G59431

phosphatidylinositol polyphosphate 5-phosphatase, isoform b [imported] - human
C;Species: Homo sapiens (man)

C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 23-Sep-2002

C;Accession: G59431; H59431; A59443; B59432; C59432; D59432; E59432; F59432

R;Duden, R.; Griffiths, G.; Frank, R.; Argos, P.; Kreis, T.E.

Cell 64, 649-665, 1991

A;Title: Beta-COP, a 110 kd protein associated with non-clathrin-coated vesicles and the Golgi complex, shows homology to beta-adaptin.

A;Reference number: G59431; MUID:91121521; PMID:1840503

A;Accession: G59431

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-893 <DUD>

A;Cross-references: GB:NP_001578; PID:g13325070; PIDN:NP_001578.2

R;Mueller, O.T.; Hartsfield, J.K. Jr.; Gallardo, L.A.; Essig, Y.P.; Miller, K.L.; Papenhausen, P.R.; Tedesco, T.A.

Am. J. Hum. Genet. 49, 804-810, 1991

A;Title: Lowe oculocerebrorenal syndrome in a female with a balanced X;20 translocation: mapping of the X chromosome breakpoint.

A;Reference number: H59431

A;Accession: H59431

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-893 <MUE>

A;Cross-references: GB:NP_001578; PID:g13325070; PIDN:NP_001578.2

R;Attree, G.; Olivos, I.M.; Okabe, I.; Bailey, L.C.; Nelson, D.L.; Lewis, R.A.; McInnes, R.R.; Nussbaum, R.L.

Nature 358, 239-242, 1992

A;Title: The Lowe's oculocerebrorenal syndrome gene encodes a protein highly homologous to inositol polyphosphate-5-phosphatase.

A;Reference number: A59443; MUID:92334430; PMID:1321346

A;Accession: A59443
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-893 <ATT>
 A;Cross-references: GB:NP_001578; PID:g13325070; PIDN:NP_001578.2
 R;Leahey, A.M.; Charnas, L.R.; Nussbaum, R.L.
 Hum. Mol. Genet. 2, 461-463, 1993
 A;Title: Nonsense mutations in the OCRL-1 gene in patients with the
 oculocerebrorenal syndrome of Lowe.
 A;Reference number: B59432; MUID:93278398; PMID:8504307
 A;Accession: B59432
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-893 <LEA>
 A;Cross-references: GB:NP_001578; PID:g13325070; PIDN:NP_001578.2
 R;Zhang, X.; Jefferson, A.B.; Auethavekiat, V.; Majerus, P.W.
 Proc. Natl. Acad. Sci. U.S.A. 92, 4853-4856, 1995
 A;Title: The protein deficient in Lowe syndrome is a phosphatidylinositol-4,5-
 bispophosphate 5-phosphatase.
 A;Reference number: C59432
 A;Accession: C59432
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-893 <ZHA>
 A;Cross-references: GB:NP_001578; PID:g13325070; PIDN:NP_001578.2
 R;Nussbaum, R.L.; Orrison, B.M.; Janne, P.A.; Charnas, L.; Chinault, A.C.
 Hum. Genet. 99, 145-150, 1997
 A;Title: Physical mapping and genomic structure of the Lowe syndrome gene OCRL1.
 A;Reference number: D59432
 A;Accession: D59432
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-893 <NUS>
 A;Cross-references: GB:NP_001578; PID:g13325070; PIDN:NP_001578.2
 R;Janne, P.A.; Suchy, S.F.; Bernard, D.; MacDonald, M.; Crawley, J.; Grinberg,
 A.; Wynshaw-Boris, A.; Westphal, H.; Nussbaum, R.L.
 J. Clin. Invest. 101, 2042-2053, 1998
 A;Title: Functional overlap between murine Inpp5b and Ocr11 may explain why
 deficiency of the murine ortholog for OCRL1 does not cause Lowe syndrome in
 mice.
 A;Reference number: E59432
 A;Accession: E59432
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-893 <JAN>
 A;Cross-references: GB:NP_001578; PID:g13325070; PIDN:NP_001578.2
 R;Erneux, C.; Govaerts, C.; Communi, D.; Pesesse, X.
 Biochim. Biophys. Acta 1436 (1-2), 185-199, 1998
 A;Title: The diversity and possible functions of the inositol polyphosphate 5-
 phosphatases.
 A;Reference number: F59432
 A;Accession: F59432
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-893 <ERN>
 A;Cross-references: GB:NP_001578; PID:g13325070; PIDN:NP_001578.2

Query Match 18.2%; Score 367.5; DB 2; Length 893;
 Best Local Similarity 29.4%; Pred. No. 3.2e-23;
 Matches 100; Conservative 58; Mismatches 131; Indels 51; Gaps 8;

```

Qy      5 SPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGKGGVNICLKLYG 64
      | : || ||: |::||:|: |:: ::|: |:: | ||||| : :
Db      307 SKAKYKKVQLVRLVGMMLLIFARKDQCRYIRDIATETVGTGIMGKMGNGKGGVAVRFVFNH 366

Qy     65 YYVSIINCHLPPHISNNYQRLEHFDRIEMQN--CEGRDIP--NILDHDLIIWFGDMNFR 120
      |:| || |:: :| : : | : : :| ||: |::|| ||:|:|
Db     367 TTFCIVNSHLAAHVEDFERRNQDYKDICARMSFVVPNQTLPLQLNIMKHEVVWLGLDNLNYR 426

Qy    121 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLFPPTYKFDRNSNDY 180
      : : | : | : |||:| : : | | : | ||||:| :: :
Db    427 LCMPDANEVKS LINKKDLQRLKFDQLNIQRTQKKA FVDFNEGEIKFIPTYKYDSKTDRW 486

Qy    181 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
      |:| | | ||| ||||| ::: | || | |||||
Db    437 DSSGKCRVPAWCDRILWR-----GTNVNQLNYRSHMELKTS DHKPVSA 529

Qy    241 TFDLELKPL-----VSAPLIVLMPEDLWTVENDMMVSYSTSDFPSSPDWIGLYKV 292
      | : :| : | : :| || : | | :|
Db    530 LFHIGVKVVDERRYRKVFELS VRIMDR---MENDFLPSLELSRREF----- 572

Qy    293 GLRDVNDYVSYAWVGDSKVSCSDNLNQVYIDISNIPTTED 332
      | : | : | :| || | || |
Db    573 ----VFENVKFRQLQKEKFQISNN-QQVPC HFSFIPKLND 607
  
```

RESULT 3

S29069

inositol polyphosphate-5-phosphatase homolog - human

C;Species: Homo sapiens (man)

C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: S29069; I68621

R;Attree, O.; Olivos, I.M.; Okabe, I.; Bailey, L.C.; Nelson, D.L.; Lewis, R.A.;
 McInnes, R.R.; Nussbaum, R.L.

Nature 358, 239-242, 1992

A;Title: The Lowe's oculocerebrorenal syndrome gene encodes a protein highly
 homologous to inositol polyphosphate-5-phosphatase.

A;Reference number: S29069; MUID:92334430; PMID:1321346

A;Accession: S29069

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-970 <ATT>

A;Cross-references: UNIPROT:Q01968

R;Leahey, A.M.; Charnas, L.R.; Nussbaum, R.L.

Hum. Mol. Genet. 2, 461-463, 1993

A;Title: Nonsense mutations in the OCRL-1 gene in patients with the
 oculocerebrorenal syndrome of Lowe.

A;Reference number: I54349; MUID:93278398; PMID:8504307

A;Accession: I68621

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 383-912 <RES>

A;Cross-references: GB:S62085; NID:g385336; PIDN:AAB26926.1; PID:g385337

C;Genetics:

Query Match 18.2%; Score 367.5; DB 2; Length 970;
Best Local Similarity 29.4%; Pred. No. 3.6e-23;
Matches 100; Conservative 58; Mismatches 131; Indels 51; Gaps 8;

```

RESULT 4
A41075
inositol-1,4,5-trisphosphate 5-phosphatase (EC 3.1.3.56) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 29-Aug-1997
C;Accession: A41075
R;Ross, T.S.; Jefferson, A.B.; Mitchell, C.A.; Majerus, P.W.
J. Biol. Chem. 266, 20283-20289, 1991
A;Title: Cloning and expression of human 75-kDa inositol polyphosphate-5-
phosphatase.
A;Reference number: A41075; MUID:92041857; PMID:1718960
A;Accession: A41075
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-672 <ROS>
A;Cross-references: GB:M74161
C;Genetics:
A;Gene: GDB:INPP5B
A;Cross-references: GDB:129756; OMIM:147264
A;Map position: 1p34-1p34
C;Keywords: phosphoric monoester hydrolase

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Query Match 16.5%; Score 334; DB 2; Length 672;
Best Local Similarity 31.7%; Pred. No. 1.6e-20;
Matches 78; Conservative 45; Mismatches 97; Indels 26; Gaps 6;

Qy 9 FIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICLKLYGYVVS 68
 : || :|: ||:|:|:| :| || : :| :| ||||| | : : :
 Db 133 YAKVKLIRLVGIMLLLYVKQEHAAYISEVEAETVGTGIMGRMGNGGGVAIRFQFHNTSIC 192

Qy 69 IINCHLPPHISNNYQRLEHF-DRILEMQNCE-GRDIP--NILDHDLIIWFGDMNFRIEDF 124
 ::| || || :| : : | || :| :| :||:|:| ||:|:|:|:
 Db 193 VVNSHLAAHIEEYERRNQDYKDICSRMQFCQPDPSLPPLTISNHDVILWLGLDNLNRIEEL 252

Qy 125 GLHFVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDYDTSE 184
 : |:: |: : : | || | : | || | | ||||:| : |
 Db 253 DVEKVKKLIEEKDFQMLYAYDQLKIQVAAKTVFEGFTEGELTFQPTYKYDTRA--LTTGI 310

Qy 185 KKRKPAWTDRI---LWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSGT 241
 | : ||: | : : | || | |||||
 Db 311 PVRSAVLLPGVIGFLWKGK-----NITQLSYQSHMALKTSDHKPVSSV 353

Qy 242 FDLELK 247
 ||: ::
 Db 354 FDIGVR 359

RESULT 5

JW0105

synaptojanin 2 alpha protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004

C;Accession: JW0105

R;Seet, L.F.; Cho, S.; Hessel, A.; Dumont, D.J.

Biochem. Biophys. Res. Commun. 247, 116-122, 1998

A;Title: Molecular cloning of multiple isoforms of synaptojanin 2 and assignment of the gene to mouse chromosome 17A2-3.1.

A;Reference number: JW0105; MUID:98300294; PMID:9636665

A;Contents: Liver

A;Accession: JW0105

A;Molecule type: mRNA

A;Residues: 1-1216 <SEE>

A;Cross-references: UNIPROT:Q9D2G5; GB:AF041862; NID:g3241994; PIDN:AAC40146.1; PID:g3241995

Query Match 16.5%; Score 334; DB 2; Length 1216;
 Best Local Similarity 31.2%; Pred. No. 3.7e-20;
 Matches 92; Conservative 49; Mismatches 124; Indels 30; Gaps 9;

Qy 9 FIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICLKLYGYVVS 68
 :| :: :|: | :| : |:|:|: : : ||: | |||| | | :|:
 Db 536 YILLTSAQLVGVCCLYIFVRPYHVPFIRDVAIDTVKTGMGGKAGNKGAVGIRFQLHSTSFC 595

Qy 69 IINCHLPPHISNNYQRLEHFDRIIL-EMQNCEGRDIPNILDHDLIIWFGDMNFRIEDFGLH 127
 : || | :| | : | : : || || || :| || |:| |
 Db 596 FVCSHLTAGQSQVKERNEDYREITHKLSFPSGR---NIFSHDYVFWCGDFNYRI-DLTYE 651

Qy 128 FVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDYDTSEKKR 187
 | :| : : | ||| : | : :| || : | ||||:| | ||||:| |
 Db 652 EVFYFVKRQDWKKLMEFDQLQLQKSSGKIFKDFHEGAVNFGPTYKYDVGSAAYDTSKCR 711

Qy 188 KPAWTDRIILWRLKRQP---CAGP---DTPI---PPASH-FSLSLRGYSSHMTYGISDHK 236
 |||||:| | :| || | : : | | :| | ||:

Db 712 TPAWTDRLVWRRKKHPYDKTAGELNLLDSDLGDGPQIRHTWSPGTLKYYGRAELQASDHR 771

Qy 237 PVSGETFDLELKPL-----VSAPLIVLMPEDLWTVENDMMVSYSSTSDFP 280
 || :|:: : ||: | | | | : :||

Db 772 PVLAIIVEVEVQEVQVGARERVFQEVSS---VQGPLDATVVVNLQSPTLEEKNEFP 823

RESULT 6

S68448

synaptojanin, 170K - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Nov-1999

C;Accession: S68448; S78547; S78527

R;McPherson, P.S.; Garcia, E.P.; Slepnev, V.I.; David, C.; Zhang, X.; Grabs, D.; Sossin, W.S.; Bauerfeind, R.; Nemoto, Y.; de Camilli, P.

Nature 379, 353-357, 1996

A;Title: A presynaptic inositol-5-phosphatase.

A;Reference number: A58183; MUID:96149250; PMID:8552192

A;Accession: S68448

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1575 <MCP>

A;Cross-references: EMBL:U45479; NID:g1166574; PIDN:AAB60525.1; PID:g1166575; PID:g1166576

A;Experimental source: brain

A;Accession: S78547

A;Molecule type: protein

A;Residues: 1075-1093;1173-1199;1290-1308 <MCS>

A;Experimental source: brain

R;de Camilli, P.

submitted to the EMBL Data Library, January 1996

A;Reference number: S78527

A;Accession: S78527

A;Molecule type: mRNA

A;Residues: 1-587,'D',589-1575 <DEC>

A;Cross-references: EMBL:U45479

C;Function:

A;Description: binds the SH3 domain of amphiphysin

C;Keywords: alternative splicing; alternative termination; synaptic vesicle

F;1-1575/Product: synaptojanin, long form b #status predicted <MAT3>

F;1-1139,1156-1575/Product: synaptojanin, long form a #status predicted <MAT2>

F;1-113,1156-1308/Product: synaptojanin, short form #status predicted <MAT1>

Query Match 16.2%; Score 328; DB 2; Length 1575;

Best Local Similarity 33.6%; Pred. No. 1.7e-19;

Matches 84; Conservative 44; Mismatches 106; Indels 16; Gaps 6;

Qy 9 FIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGGGVNICLKLYGYVVS 68
 :: :: :: | : | | : | | | : : : : | : | | | | | : : :
 Db 625 YVLLASEQLVGVCLFVFIRPQHAPFIRDVAVDTVKTMGGATGNKGAVAIRMLFHTTSLC 684

Qy 69 IINCHLPPHISNNYQRLEHFDRIIL-EMQNCCEGRDIPNILDHDLIIWFGDMNFRIEDFGLH 127
 : | : | : | | : : | : | : | | | : | | |
 Db 685 FVCSHFAAGQSQVKERNEDFVEIARKLSFPMGR---MLFSHDYVFWCGDFNYRI-DLPNE 740

Qy 128 FVRESIKNRCYGGWLWEKDQLSIAKKHDPLREFQEGRLLPPTYKFDRNSNDYDTSEKKR 187
 | : | : : : | | | : | | | : : | | | : | | | | |

Db 741 EVKELIRQQNWDSL IAGDQLINQKNAGQIFRGFLEGKVTFAPTYKYDLFSEDYDTSEKCR 800

Qy 188 KPAWTDRLWLRLKRQPC--AGPDTPIPPASHFSLSLRGYS----SHMTYG-----ISDHK 236
 |||||:|||| :: | : | : || | : : || |||:

Db 801 TPAWTDRLWRRRKWPFDRSAEDLDLLNASFQDESKILYTWTPGTLHYGRAELKTS DHR 860

Qy 237 PVS GTFDLEL 246
 || |:::

Db 861 PVVALIDIDI 870

RESULT 7

D86190

hypothetical protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: D86190

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hocper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, A.; Militscher, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, E.I.; Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D86190

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1136 <STO>

A;Cross-references: UNIPROT:Q9SYK4; GB:AE005172; NID:g4836913; PIDN:AAD30615.1; GSPDB:GN00141

C;Genetics:

A;Map position: 1

Query Match 15.3%; Score 309.5; DB 2; Length 1136;
 Best Local Similarity 27.3%; Pred. No. 4.3e-18;
 Matches 93; Conservative 52; Mismatches 109; Indels 87; Gaps 11;

Qy 8 SFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNKGGVNICLKLYGYV 67
 :| :: :: |:|: ::|: :: | : | | ||||| : ::| :

Db 651 TFERMGSRLAGLLISLWARKDIRTHVGDLDVAAPCGFGRAGNKGGLRIRVYDRIM 710

Qy 68 SIINCHLPPHIS-----NNYQRLEHFDRIEMQNC-----EGRDIP--- 103
 :||| | : | : || | : | : ||

Db 711 CFVNCHLAAHLEAVNRRNADFNHIFRLMVFSRGQNLNAAAAGVSTSAYTTKSNTIPSTG 770

Qy 104 -----NILDHDLIIWFGDMNFRIEDFGLHF--VRESIKNRCYGGLWEKDQLSIAKKHDP 155
 :: |:: :||| |:: |:: : | : | : | :||| |
 Db 771 AEEIKSDLAAADMVAFFGDFNYRL--FGITYDEARDFISQRSFDWLRERDQLRAEMKVGK 828

Qy 156 LLREFQEGRLLPPTYKFDRNSN---DYDTSEKKRKPAWTDRLWRLKRQPCAGPDTPIP 212
 : : :| : |||||::|| : ||: |||| ||| ||:::| ||
 Db 829 VFQGMREALITFPPTYKFERNRSGLGGYDSGEKKRIPAWCDRVIYR-----DTQSS 879

Qy 213 PASHFSL-----SLRGYSSHMTYGISDHKPVSGTF----- 242
 | | :| : | : | ||||| |
 Db 880 PFSESNLQCPVSVIMYEACMDVTESDHKPVRCCKFHATIAHVDKSVRRQELGKIIRSNE 939

Qy 243 -----DLELKP--LVSAPLIVLMPED--LWTVENDMMVS 272
 || | || || :| : | : |
 Db 940 KILSIFEDLRFVPETSVSTNNIVLQSQDTVILTITNNSPTS 980

RESULT 8

T00670

probable inositol polyphosphate 5'-phosphatase [imported] - Arabidopsis thaliana
 N;Alternate names: hypothetical protein F6E13.3

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C;Accession: T00670; H84871

R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
 Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.;
 Venter, J.C.

submitted to the EMBL Data Library, June 1998

A;Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.

A;Reference number: Z14180

A;Accession: T00670

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1305 <ROU>

A;Cross-references: UNIPROT:O80560; EMBL:AC004005; NID:g3212846; PID:g3212848

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;
 Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell,
 C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin,
 L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams,
 M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhagen,
 G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser,
 C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84871

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1305 <STO>

A;Cross-references: GB:AE002093; NID:g3212848; PIDN:AAC23399.1; GSPDB:GN00139

C;Genetics:

A;Gene: F6E13.3; At2g43900

A;Map position: 2

A;Introns: 278/1; 362/2; 631/3; 674/2; 702/3; 758/1; 771/3; 861/1; 902/2; 1022/3

Query Match 15.1%; Score 306; DB 2; Length 1305;
Best Local Similarity 27.1%; Pred. No. 1e-17;
Matches 76; Conservative 55; Mismatches 97; Indels 52; Gaps 7;

```
Qy      9 FIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICLKLYGYYVS 68
      | ::  :: |:|: :: :  :: :  : | |  ||||| : :::: :
Db      558 FERMGSRLAGLLISLWVRKNLRTHVGDIDVAAPCGFGRAIGNKGGVGLRIRVFDRIMC 717

Qy      69 IINCHLPPHISNNYQRLEHFDRILE----MQNCEGRDIP----- 103
      ||||| |:  :|  || | :  ::  : |
Db      718 FINCHLAAHLEAVNRRNADFDHIYKTMSFTRSSNAHNAPAAGVSTGSHTTKSANNANVNT 777

Qy     104 -----NILDHDLIIWFGDMNFRIEDFGLHF--VRESIKNRCYGGGLWEKDQLSIAKKHDPL 156
      :: : |:::|||| |:|: ||: :  |: :  | :  |||||  | :
Db     778 EETKQDLAEADMVVFVFGDFNYRL--FGISYDEARDFVSQRSFDWLREKDQLRAEMKAGRV 835

Qy     157 LREFQEGRLLPPTYKFDNRNS---NDYDTSEKKRKPATDRILWRLKRQPCAGPDTPIPP 213
      : :| : ||||| |:|:  ||: ||| ||| ||::|  ||  |
Db     836 FQGMREAIITFPPTYKFERHRPGLGGYDSGEKKRIPAWCDRVIFR-----DTRTSP 886

Qy     214 ASHFSL-----SLRGYSSHMTYGISDHKPVSGTFDLELK 247
      | |  | :  | :  |||||  | ::::
Db     887 ESECSLDCPVVASIMLYDACMDVTESDHKPVRCFKFHVKIE 926
```

RESULT 9

T19338

hypothetical protein C16C2.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T19338

R;Barlow, K.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19109

A;Accession: T19338

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-753 <WIL>

A;Cross-references: UNIPROT:O17590; EMBL:Z81036; PIDN:CAB02743.1; GSPDB:GN00019;

CESP:C16C2.3

A;Experimental source: clone C16C2

C;Genetics:

A;Gene: CESP:C16C2.3

A;Map position: 1

A;Introns: 17/1; 36/2; 88/2; 131/2; 170/3; 268/3; 389/2; 475/3; 498/3; 632/1;
677/2; 713/1

Query Match 14.9%; Score 300.5; DB 2; Length 753;
Best Local Similarity 31.1%; Pred. No. 1.4e-17;
Matches 85; Conservative 40; Mismatches 93; Indels 55; Gaps 9;

```
Qy      9 FIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTG---LFGYWGNGGGVNICLKLYGY 65
      | |  :|: || ::||  :  :: |  ||  |  ||||| : :|:
Db     168 FNVVGSMLVGIFVIVFQAVNSKVRVSDVNVKYVATGISVLVNKLGNKGGTAVSMKMNDT 227

Qy     66 YVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPN----- 104
      :|  :| |  ||  || :| : ||| |
```


Db 228 WVCVNAHFA--AGNNE-----LERRNQDFRDIYNDMVFYPRSQQEGLRDRPLEVP 276

Qy 105 ---ILDHDLIIWFGDMNFRI--EDFGL--HFVRESIKNRCYGGLWEKDQLSIAKKHDPLL 157
 : |||:: ||||:|:|: : :|: || : : | : || :

Db 277 IMCLYDHDVVFWFGLNRYRLNTDMYGISNDEVRRIASSDKFADLLQHCQLREQMARGTVF 336

Qy 158 REFQE-GRLLFPPTYKFDRNSNDYDTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASH 216
 ::|:| | | ||||:| :| :|||| | ||||| | :| | | :

Db 337 KDFEEPSTLPFRPTYKYDCGTNTWDTSEKGRVPAWTDRL-TFKKYPQVGLE----- 387

Qy 217 FSLSLRGYSSHMTYGISDHKPVSGTFDLELKPL 249
 |:| | | ||||| | |:|::| :

Db 388 ---SIRPMVSIDTITISDHKPVAMFNLKVKKI 417

RESULT 10

D96515

hypothetical protein F16N3.22 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: D96515

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.D.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.

Nature 403, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Militscher, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D96515

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-331 <STO>

A;Cross-references: UNIPROT:Q9SX81; GB:AE005173; NID:g5668810; PIDN:AAD46036.1; GSPDB:GN09141

C;Genetics:

A;Gene: F16N3.22

A;Map position: 1

Query Match 14.8%; Score 298.5; DB 2; Length 331;
 Best Local Similarity 34.4%; Pred. No. 6.8e-18;
 Matches 83; Conservative 33; Mismatches 90; Indels 35; Gaps 9;

Qy 16 RMQGILLLVFA-KYQHLPYIQILSTKSTPTGLFGYWG-NKGGVNICLKLYGYYSIINCH 73
 ::| : | :| | | : : : : | | | | | : : |:| |

Db 113 KLQSVQLYLFGPKNSHTLVKELKAERYSVGGCGGLIGRKKGAFAIRINYDDIKMVFISCH 172

Qy 74 LPPHISNNYQRLEHFDRILEMQNCEGRDIPNIL-----DHDLIWFGDMNFRIEDFGLH 127
 | | : : | | | | | | : | | : | : | : | |
 Db 173 LSAHAKK-----VDQRNTELRHIANSLPRDKRKRDLTVWLGDLDNYRIQDVSNH 221

Qy 128 FVRESIKNRCYGGWLEKDQLSIAKKHDPLLREFQEGRLFPPTYKFDRNSNDYDTSEKKR 187
 | | | : | | | | : : : | | | | | | : | : | | | | |
 Db 222 PVRSLIQNHLQSVLVSKDQLLQEAERGEIFKGYSEGTLGFKPTYKYNVGSSDYDTSHKIR 281

Qy 188 KPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSS-HMTYGISDHKPVSGTFDLEL 246
 | | | | | | : : : | | : : | | | | | | | | | | |
 Db 282 VPAWTDRLFKIQ-----DT-----DNIQATLHSYDSIDQVYG-SDHKPVKA--DLCL 326

Qy 247 K 247
 |
 Db 327 K 327

RESULT 11

G84792

hypothetical protein At2g37440 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: G84792

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: G84792

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-401 <STO>

A;Cross-references: UNIPROT:Q9ZUS3; GB:AE002093; NID:g4056496; PIDN:AAC98062.1; CSPDB:GN00139

C;Genetics:

A;Gene: At2g37440

A;Map position: 2

Query Match 14.7%; Score 297.5; DB 2; Length 401;
 Best Local Similarity 29.7%; Pred. No. 1.1e-17;
 Matches 76; Conservative 43; Mismatches 98; Indels 39; Gaps 7;

Qy 6 PLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNKGGVNICLKLYGY 65
 | : : : | | | : : | | : | | | | : | : | :
 Db 113 PRGYSLAASKQMVGFILCVWVRDDLRLKRNITNLKVCVGRGIMGYLGNGKGSVSISMSLHET 172

Qy 66 YVSIINCHLP-----PHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIWFGDMNF 119
 : : | : | | : : : : | : | | : | | : | : | :
 Db 173 SLCFVCTHLTSGEKEGDELRRNLDVTEIFKRTFRSSKDSRPETIMDHDKVIWLGDLNY 232

| | | | |
|----|-----|--|-----|
| Qy | 120 | RIE-DFGLHVFRESIKNRCYGGLWEKDQLSIAKKHDPLLREFQEGRLLFPPTYKFDRNSN | 178 |
| | | : :: : :: : : :: :: : : | |
| Db | 233 | RLRASSDLH---EQLRNHDWESLLEKDLKIEQRAGRIFKGWEEGKIYFAPTYKYRINS | 289 |
| Qy | 179 | DY-----DTSEKKRKPAWTDRLWR---LKRQPCAGPDTPIPPASHFSLSLRGYSSHMTY | 230 |
| | | : : : : : : : | |
| Db | 290 | NYVVQTEKSKEKRRTPAWCDRLWKGDGMKQ-----LWYVRGESK---- | 329 |
| Qy | 231 | GISDHKPVSGTFDLEL | 246 |
| | | : : : | |
| Db | 330 | -FSDHRPVQSLFSVHI | 344 |

RESULT 12

S61667

probable membrane protein YOR109w - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein 03231; hypothetical protein YOR3231w

C;Species: *Saccharomyces cerevisiae*

C;Date: 09-Mar-1996 #sequence revision 12-Apr-1996 #text change 09-Jul-2004

C;Accession: S61667; S66994

R; Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banrevi, A.; Sander, C.; Valencia, A.; Ansorge, W.; Voss, H.

submitted to the EMBL Data Library, December 1995

A;Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome XV.

A;Reference number: S61643

A;Accession: S61667

A; Molecule type: DNA

A;Residues: 1-1107 <BEN>

A;Cross-references: UNIPROT:Q12271; EMBL:X94335; NID:g1262139; PID:g1164954

R. VOSS, H.; BENES, V.; RECHMANN, S.; TEODORU, C.; SCHWAGER, C.; PACES, V.;
ANSORGE, W.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66955

A;Accession: S66994

A;Molecule type: DNA

A;Residues: 1-1107 <VOS>

A;Cross-references: EMBL:Z75017; NID:g1420294; PID:g1420295; MIPS:YOR109w

A; Experimental source: strain S288C

C; Genetics:

A; Gene: SGD:INP53

A;Cross-references: SGD:S0005635; MIPS:YOR109w

A;Map position: 15R

C; Keywords: transmembrane protein

7;60-76/Domain: transmembrane #status predicted <TM1>

F;642-658/Domain: transmembrane #status predicted <TM2>

Query Match 14.4%; Score 291.5; DB 2; Length 1107;

Best Local Similarity 26.8%; Pred. No. 1.5e-16;

Matches 98; Conservative 57; Mismatches 141; Indels 69; Gaps 12;

| | | | |
|----|-----|--|-----|
| Qy | 15 | RMQGILLLVFAKYQHLPIYQILSTKSTPTGLFGYWGNGKGVNICLKLYGYVYSIINCHLP | 75 |
| | | : : : :: : : ! : : : | |
| Db | 648 | QMTSLILFFVKADKAKYVKQVEGATKKTGFRGMAGNKGAVSIRFEYGATSFCFVNSHLA | 707 |
| Qy | 76 | PHISNNYQRLEHFDRILE-MQNCEGRDIPNILDHDLIIWFGDMNFRI---EDFGLHFVR | 130 |
| | | : : :: : : : : : | |

| | | | |
|----|-----|--|-----|
| Db | 708 | AGATNVEERRSDYESIVRGITFTRTKMIPH---HDSIFWLGDMMYRINLPNED-----VR | 759 |
| Qy | 131 | ESIKNRCYG---GLWEKDQLSIKKHDPDLLREFQEGRLFPPTYKFDRNSNDYDTSEKKR | 187 |
| | | : : :: : : : : : : | |
| Db | 760 | RELLNQEEGYIDKLLHFDQLTLGINSQSVFEGFKEPTLKFRPTYKYDPGTGTYSSEKER | 819 |
| Qy | 188 | KPAWTDRIWLRLKR-QPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSGTF---- | 242 |
| | | : : : ::: : : : : : | |
| Db | 820 | TPSWTDRIIYKGENLLPLSYSDAPIM-----ISDHRPVYAAAYRAKI | 860 |
| Qy | 243 | -----DLELKPLVSAPLIVLMPEDLWTVENDMM---VSYSSTSDFPSPPWDWIGLYKV | 292 |
| | | : : :: : : : : : | |
| Db | 861 | TFVDDKERLSLKKRLFTEYKQEHPEEPGSLISDLLSLDLDNKSTDGFKSSS-----ES | 913 |
| Qy | 293 | GLRDVNDYVSYAWVGDSKVSQSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRP | 352 |
| | | : :: : : :: : : : : | |
| Db | 914 | SLLDIDPIMAQPTA--SSVASSSPVSSASASLQPVRT-----QNSSQSRTPIKKP | 961 |
| Qy | 353 | FQIPP 357 | |
| | | | |
| Db | 962 | VLRPP 966 | |

RESULT 13

S48433
inositol-1,4,5-trisphosphate 5-phosphatase homolog YIL002c -- yeast
(*Saccharomyces cerevisiae*)
N;Alternate names: protein YIA2c
C;Species: *Saccharomyces cerevisiae*
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: S48433; S58703; S50873
R;Badcock, K.; Churcher, C.
submitted to the EMBL Data Library, August 1994
A;Reference number: S48432
A;Accession: S48433
A;Molecule type: DNA
A;Residues: 1-946 <BAD>
A;Cross-references: UNIPROT:P40559; GB:Z47047; EMBL:Z38062; NID:g603997;
PID:g763344; MIPS:YIL002c
R;Voss, H.
submitted to the EMBL Data Library, June 1994
A;Reference number: S58703
A;Accession: S58703
A;Molecule type: DNA
A;Residues: 1-946 <VOS>
A;Cross-references: EMBL:X79743
R;Voss, H.; Tamames, J.; Teodoru, C.; Valencia, A.; Sensen, C.; Wiemann, S.;
Schwager, C.; Zimmermann, J.; Sander, C.; Ansorge, W.
Yeast 11, 61-78, 1995
A;Title: Nucleotide sequence and analysis of the centromeric region of yeast
chromosome IX.
A;Reference number: S50795; MUID:95282515; PMID:7762303
A;Accession: S50873
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 650-820 <VOW>
A;Cross-references: EMBL:X79743

C;Genetics:
A;Gene: SGD:INP51
A;Cross-references: SGD:S0001264; MIPS:YIL002c
A;Map position: 9L
C;Keywords: transmembrane protein
F;71-87/Domain: transmembrane #status predicted <TMM>

Query Match 14.3%; Score 289.5; DB 2; Length 946;
Best Local Similarity 31.5%; Pred. No. 1.7e-16;
Matches 90; Conservative 38; Mismatches 115; Indels 43; Gaps 8;

```

Qy      9 FIKVSHVRMQGILLLVFAKYQHLPYIQLSTKSTPTGLFGYWGNKGGVNICKLYGYVVS 68
      :|::  :: |||||:|  :: :  || |  ||| | : |
Db      607 YIRLWSTQLGGILLLLFMNETEYSKVKHIEGDVKKTGFGGMASNKGAVAVSFKYSATRFC 666

Qy      69 IINCHLPPHISNNYQRLEHFDRIE-MQNCEGRDIPNILDHDLIIWFGDMNFRI----ED 123
      :: ||  : |  ||  : | : :: :|  ||| ||| || |::|  ||
Db      667 VLVSHLAAGLENVEQRHNDYKTIAKSIRFSKGL---RIKDHDALIIWMGDFNYRILMSNED 723

Qy      124 FGLHVFVRESIKNRCYGGLWEKDQLS---IAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
      || | :: | |::|||:  || : |  | : ||||| | : :|
Db      724 -----VRRKIVSKEYASLFEKDQLNQMIAGESFPY---FHEMAIDFPPTYKFDPGTKNY 775

Qy      181 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
      ||||| | ||||| | :  |  |  |||:|
Db      776 DTSEKMRIPAWTDRLSRGE-----VLEQLEYKCCEDILFSDHRPVYA 818

Qy      241 TF-----DLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDF 279
      |  : | : : : | | : : |  |
Db      819 IFRARVTVVDEQKKTTLGTQIYEKIMERLEGLDDDEKIAVLSDDAF 864

```

RESULT 14

F84725

probable inositol polyphosphate 5'-phosphatase [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004.

C;Accession: F84725

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: F84725

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1144 <STO>

A;Cross-references: UNIPROT:Q9SKB7; GB:AE002093; NID:g4887753; PIDN:AAD32289.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g31830

A;Map position: 2

Query Match 14.1%; Score 284; DB 2; Length 1144;
Best Local Similarity 27.4%; Pred. No. 6.8e-16;
Matches 75; Conservative 49; Mismatches 94; Indels 56; Gaps 8;

```
Qy      8 SFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNKGGVNICLKLYGYV 67
      :| ::  :: |:|: :: :  :: |  : |  |||||: ::| :
Db      660 TFERMGSRLAGLLISLWVRKSIRTHVGDLDVAAPCGFGRAIGNKGGVGLRIRVYDRIM 719

Qy      68 SIINCHLPPHISNNYQRLEHFDRIL-EMQNCEGRDI-----PN---- 104
      :||| | :  :|  |: |  |  :|: :  ||
Db      720 CFVNCHLAAHLEAVTRRNADFNHIYRSMVFSKGQSVYTAAAAGASTSAQALKNNPNTNNS 779

Qy      105 -----ILDHDLIIWFGDMNFRIEDFGLHF--VRESIKNRCYGGWLWEKDQLSIKKHDP 155
      :  ||: :||| |:|: ||: :  |: | :| : | ||||
Db      730 TEEKSHLASADLVAFFGDFNYRL--FGITYDEARDFISHRSFDWLREKDQLRQEMNEGK 837

Qy      156 LLREFQEGRLLEFPPTYKFDRNS---NDYDTSEKKRKPAWTDRLWRLKRQPCAGPDTPIP 212
      : : :| : |||||:|: ||: ||| ||| ||::| :
Db      838 VFQGMREALITFPPTYKFEKNKPGGGYDSGEKKRIPAWCDRVIYRDNQS----- 887

Qy      213 PASHFSLSLR-----GYSSHMTYGISDHKPV 238
      |: ||: | : | |||||
Db      888 -ISYTECSLKCPVVSSTIMYEACMDVTESDHKPV 920
```

RESULT 15

JC5765

inositol polyphosphate 5-phosphatase (EC 3.1.3.-) 2 - human

C;Species: Homo sapiens (man)

C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004

C;Accession: JC5765

R;Pesesse, X.; Deleu, S.; De Smedt, F.; Drayer, L.; Erneux, C.

Biochem. Biophys. Res. Commun. 239, 697-700, 1997

A;Title: Identification of a second SH2-domain-containing protein closely related to the phosphatidylinositol polyphosphate 5-phosphatase SHIP.

A;Reference number: JC5765; MUID:98042455; PMID:9367831

A;Accession: JC5765

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1258 <PES>

A;Cross-references: UNIPROT:O15357; GB:Y14385; NID:g2653423; PIDN:CAA74743.1;

PID:c1188709; PID:g2653424

C;Comment: This enzyme plays a role in metabolism of inositol phosphate and phosphatidylinositol.

C;Keywords: phosphoric monoester hydrolase

F;21-117/Domain: SH2 homology <SH2>

F;427-729/Domain: catalytic #status predicted <CAT>

F;927-1171/Region: proline-rich

Query Match 14.1%; Score 284; DB 2; Length 1258;
Best Local Similarity 25.0%; Pred. No. 7.7e-16;
Matches 96; Conservative 66; Mismatches 154; Indels 68; Gaps 14;

```
Qy      4 LSPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNKGGVNICLKLY 63
      |: | : :: : | : | | : | :|| | ||: ||| | :
```

Db 492 LTDLDIRPIAMQSLWNIKVAVLVKPEHENRISHVSTSSVKTGIANTLGNGAVGVVSFMMN 551

Qy 64 GYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDL----IIWFGDMNF 119
| : ||| : : : | : | | : ||| : :

Db 552 GTSFGFVNCHLTSGNEKTARRNQNYLDILRLSLGDRQL-NAFDISLRFTHLFWFGDLNY 610

Qy 120 RIEDFGLHFVRESIKNRCYGGWLEKDQLSIAK-KHDPLLREFQEGRLFPPTYKFDRNSN 178
| : | : : | : : | || : : | | | : ||| : : |

Db 611 RL-DMDIQEILNYISRKEFEPLLRVDQLNLEREKHKVFLR-FSEEEISFPPTYRYERGSR 668

Qy 179 D-----YDTSEKKRKPATWDRILWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYG 231
| : : | : | ||| : : | : | : : :

Db 669 DTYAWHKQKPTGVRTNPVPSWCDRILWKS-----PETHIICNSYGCTDDIV-- 714

Qy 232 ISDHKPVSGTFDLELKPLVSAPLIVLMPEDLWTV-----NDMMVSYSSSTSDFPSSPWDWIG 288
||| || ||| : : : : : | : | : : | : | : :

Db 715 TSDHSPVFGTFEVGVTSQFISKGLSKTSDQAYIEFESIEAIVKTASRTKF-----FIE 768

Qy 289 LYKVGLRDVNDYVSYAWVGDSKVSCLNQLNQVYIDISN--IPT-----TEDEFLL 336
| | : : : : ||| : : | : : | : : |

Db 769 FYSTCLEE-----YKKSFENDAQSSDNINFLKVQWSSRQLPTLKPILADIEYLQDQHL 322

Qy 337 CYYSN-----SLRSVVG 348
: : | : : |

Db 323 LTVKSMGDGYESYGECVVALKSMIG 846

Search completed: February 10, 2005, 17:50:42
Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 17:38:56 ; Search time 176 Seconds
(without alignments)
1082.349 Million cell updates/sec

Title: US-09-892-287-1
Perfect score: 2020
Sequence: 1 MDVLSPLSFIVKSHVRMQGI.....FQIPPGSLREDPLGEAQPQI 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|------------|--------------------|
| 1 | 2010 | 99.5 | 448 | 1 | SKIP_HUMAN | Q9bt40 homo sapien |
| 2 | 1525 | 75.5 | 468 | 1 | SKIP_MOUSE | Q8c5l6 mus musculu |
| 3 | 1115 | 55.2 | 496 | 2 | Q6GN99 | Q6gn99 xenopus lae |
| 4 | 873.5 | 43.2 | 1003 | 1 | P5PA_MOUSE | P59644 mus musculu |
| 5 | 872.5 | 43.2 | 1001 | 1 | P5PA_RAT | Q9jmc1 rattus norv |
| 6 | 870.5 | 43.1 | 638 | 2 | Q6ZTH6 | Q6zth6 homo sapien |
| 7 | 864.5 | 42.8 | 1006 | 1 | P5PA_HUMAN | Q15735 homo sapien |
| 8 | 516 | 25.5 | 501 | 2 | Q7PYY6 | Q7pyy6 anopheles g |
| 9 | 507.5 | 25.1 | 508 | 2 | Q9VXE7 | Q9vxe7 drosophila |
| 10 | 460.5 | 22.8 | 357 | 2 | Q9V7X0 | Q9v7x0 drosophila |
| 11 | 432.5 | 21.4 | 736 | 2 | Q86YE1 | Q86ye1 homo sapien |
| 12 | 432.5 | 21.4 | 748 | 2 | Q6PD53 | Q6pd53 homo sapien |
| 13 | 432.5 | 21.4 | 871 | 2 | Q6P6D4 | Q6p6d4 homo sapien |
| 14 | 432.5 | 21.4 | 942 | 1 | I5P2_HUMAN | P32019 homo sapien |
| 15 | 423.5 | 21.0 | 742 | 2 | Q8CF65 | Q8cf65 mus musculu |
| 16 | 423.5 | 21.0 | 757 | 2 | Q9DBW2 | Q9dbw2 mus musculu |
| 17 | 423.5 | 21.0 | 776 | 2 | O54996 | O54996 mus musculu |
| 18 | 423.5 | 21.0 | 825 | 2 | Q91ZF8 | Q91zf8 mus musculu |
| 19 | 423.5 | 21.0 | 993 | 2 | Q8K337 | Q8k337 mus musculu |
| 20 | 334 | 19.0 | 787 | 2 | Q8I7P3 | Q8i7p3 dictyosteli |
| 21 | 373.5 | 18.5 | 727 | 2 | Q8BXC9 | Q8bxc9 mus musculu |
| 22 | 373.5 | 18.5 | 900 | 2 | Q6NVF0 | Q6nvf0 mus musculu |
| 23 | 372 | 18.4 | 511 | 2 | Q8BXT3 | Q8bxt3 mus musculu |
| 24 | 367.5 | 18.2 | 901 | 1 | OCRL_HUMAN | Q01968 homo sapien |
| 25 | 341.5 | 16.9 | 1800 | 2 | Q8I7P5 | Q8i7p5 dictyosteli |
| 26 | 340 | 16.8 | 1113 | 2 | Q9XUD3 | Q9xud3 caenorhabdi |
| 27 | 340 | 16.8 | 1119 | 2 | Q9GT42 | Q9gt42 caenorhabdi |
| 28 | 339 | 16.8 | 1101 | 2 | Q84W55 | Q84w55 arabidopsis |
| 29 | 339 | 16.8 | 1291 | 2 | Q9DGN7 | Q9dgn7 lampetra fl |
| 30 | 338 | 16.7 | 1101 | 2 | Q9XFT1 | Q9xft1 arabidopsis |
| 31 | 335 | 16.6 | 1273 | 2 | Q7Q001 | Q7q001 anopheles g |
| 32 | 334 | 16.5 | 1434 | 1 | SYJ2_MOUSE | Q9d2g5 mus musculu |
| 33 | 328 | 16.2 | 552 | 2 | Q6AVN0 | Q6avn0 oryza sativ |
| 34 | 328 | 16.2 | 1315 | 2 | O94984 | O94984 homo sapien |
| 35 | 328 | 16.2 | 1574 | 1 | SYJ1_MOUSE | Q8chc4 mus musculu |
| 36 | 328 | 16.2 | 1574 | 1 | SYJ1_RAT | Q62910 rattus norv |
| 37 | 328 | 16.2 | 1575 | 1 | SYJ1_HUMAN | O43426 homo sapien |
| 38 | 327.5 | 16.2 | 1288 | 2 | Q8IZA8 | Q8iza8 homo sapien |
| 39 | 327.5 | 16.2 | 1443 | 1 | SYJ2_HUMAN | O15056 homo sapien |
| 40 | 327.5 | 16.2 | 1496 | 2 | Q9H226 | Q9h226 homo sapien |
| 41 | 326 | 16.1 | 1248 | 1 | SYJ2_RAT | O55207 rattus norv |
| 42 | 326 | 16.1 | 1451 | 2 | Q91ZD9 | Q91zd9 rattus norv |
| 43 | 326 | 16.1 | 1496 | 2 | Q91ZD8 | Q91zd8 rattus norv |

| | | | | | | |
|----|-------|------|------|---|------------|--------------------|
| 44 | 325 | 16.1 | 1324 | 1 | SYJ1_BOVIN | O18964 bos taurus |
| 45 | 320.5 | 15.9 | 1107 | 2 | Q6ZK18 | Q6zk18 oryza sativ |

ALIGNMENTS

RESULT 1

SKIP_HUMAN

ID SKIP_HUMAN STANDARD; PRT; 448 AA.

AC Q9BT40; Q15733; Q9NPJ5; Q9P2R5;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Skeletal muscle and kidney enriched inositol phosphatase

DE (EC 3.1.3.56).

GN Name=SKIP; Synonyms=PPS;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND TISSUE

RP SPECIFICITY.

RC TISSUE=Testis;

RX MEDLINE=20219123; PubMed=10753883; DOI=10.1074/jbc.275.15.10870;

RZ Ijima T., Mochizuki Y., Fukami K., Funaki M., Asano T., Takenawa T.;

RT "Identification and characterization of a novel inositol polyphosphate

RT 5-phosphatase.";

RL J. Biol. Chem. 275:10870-10875(2000).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Eye;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RP SEQUENCE OF 120-448 FROM N.A.

RC TISSUE=Brain;

RA Nussbaum R.L.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SUBCELLULAR LOCATION, AND MUTAGENESIS OF TYR-349; ASP-361; TRP-362 AND
 RP TYR-376.
 RX MEDLINE=22538472; PubMed=12536145; DOI=10.1074/jbc.M209991200;
 RA Gurung R., Tan A., Ooms L.M., McGrath M.J., Huysmans R.D.,
 RA Munday A.D., Prescott M., Whisstock J.C., Mitchell C.A.;
 RT "Identification of a novel domain in two mammalian inositol-
 RT polyphosphate 5-phosphatases that mediates membrane ruffle
 RT localization. The inositol 5-phosphatase SKIP localizes to the
 RT endoplasmic reticulum and translocates to membrane ruffles following
 RT epidermal growth factor stimulation.";
 RL J. Biol. Chem. 278:11376-11385(2003).
 CC -!- FUNCTION: Inositol 5-phosphatase which acts on inositol 1,4,5-
 CC trisphosphate, inositol 1,3,4,5-tetrakisphosphate,
 CC phosphatidylinositol 4,5-bisphosphate and phosphatidylinositol
 CC 3,4,5-trisphosphate. Has 6-fold higher affinity for
 CC phosphatidylinositol 4,5-bisphosphate than for inositol 1,4,5-
 CC trisphosphate. May negatively regulate assembly of the actin
 CC cytoskeleton.
 CC -!- CATALYTIC ACTIVITY: D-myo-inositol 1,4,5-trisphosphate + H(2)O =
 CC myo-inositol 1,4-bisphosphate + phosphate.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum. Following stimulation
 CC with EGF, translocates to membrane ruffles.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9BT40-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9BT40-2; Sequence=VSP_050612;
 CC -!- TISSUE SPECIFICITY: Ubiquitously expressed with highest levels in
 CC skeletal muscle, heart and kidney.
 CC -!- SIMILARITY: Belongs to the inositol-1,4,5-trisphosphate 5-
 CC phosphatase type II family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB036829; BAA92340.1; -.
 DR EMBL; AB036830; BAA92341.1; -.
 DR EMBL; AB036831; BAA92342.1; -.
 DR EMBL; BC004362; AAH04362.1; -.
 DR EMBL; U45973; AAB03214.1; -.
 DR HSSP; O43001; 1I9Z.
 DR MIM; 607875; -.
 DR GO; GO:0005829; C:cytosol; ISS.
 DR GO; GO:0043005; C:neuronal cell projection; ISS.
 DR GO; GO:0016312; F:inositol bisphosphate phosphatase activity; ISS.
 DR GO; GO:0046030; F:inositol trisphosphate phosphatase activity; ISS.
 DR GO; GO:0042577; F:lipid phosphatase activity; ISS.
 DR GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; ISS.

DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPPc.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR SMART; SM00128; IPPc; 1.
 KW Alternative splicing; Endoplasmic reticulum; Hydrolase.
 FT DOMAIN 16 318 Catalytic (Potential).
 FT DOMAIN 321 448 Required for ruffle localization.
 FT VARSPLIC 1 76 Missing (in isoform 2).
 FT /FTid=VSP_050612.
 FT MUTAGEN 349 349 Y->A,F: No effect on EGF-induced ruffle
 FT localization.
 FT MUTAGEN 361 361 D->A: Significant decrease in EGF-induced
 FT ruffle localization.
 FT MUTAGEN 362 362 W->A: Significant decrease in EGF-induced
 FT ruffle localization.
 FT MUTAGEN 376 376 Y->A,F: No effect on EGF-induced ruffle
 FT localization.
 FT CONFLICT 120 120 T -> A (in Ref. 3).
 FT CONFLICT 416 416 R -> S (in Ref. 2).
 FT CONFLICT 426 426 R -> S (in Ref. 2).
 SQ SEQUENCE 448 AA; 51228 MW; 0651BE3C6E2EEB0F CRC64;

Query Match 99.5%; Score 2010; DB 1; Length 448;
 Best Local Similarity 99.5%; Pred. No. 1.1e-164;
 Matches 370; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWCNKGGVNICL 60
      |||
Db      77 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWCNKGGVNICL 136

Qy      61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
      |||
Db      137 KLYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 196

Qy      121 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLFPPTYKFDRNSNDY 180
      |||
Db      197 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPLLREFQEGRLLFPPTYKFDRNSNDY 256

Qy      181 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
      |||
Db      257 DTSEKKRKPAWTDRIWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 316

Qy      241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY 300
      |||
Db      317 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVNDY 376

Qy      301 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNLSRVSVGISRPFQIPPGSL 360
      |||
Db      377 VSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNLSRVSVGIRPFQIPPGSL 436

Qy      361 REDPLGEAQPQI 372
      |||
Db      437 REDPLGEAQPQI 448

```

RESULT 2
 SKIP_MOUSE

ID SKIP_MOUSE STANDARD; PRT; 468 AA.
AC Q8C5L6; 009040;
DT 10-OCT-2003 (Rel. 42, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Skeletal muscle and kidney enriched inositol phosphatase
DE (EC 3.1.3.56).
GN Name=Skip; Synonyms=Pps;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97325785; PubMed=9182797; DOI=10.1016/S0896-6273(00)80312-8;
RA Hamilton B.A., Smith D.J., Mueller K.L., Kerrebrock A.W.,
RA Bronson R.T., van Berkel V., Daly M.J., Kruglyak L., Reeve M.P.,
RA Nemhauser J.L., Hawkins T.L., Rubin E.M., Lander E.S.;
RT "The vibrator mutation causes neurodegeneration via reduced expression
RT of PITP alpha: positional complementation cloning and extragenic
RT suppression.";
RL Neuron 18:711-722(1997).
RN [2]
RP SEQUENCE FROM N.A..
RC STRAIN=ILS, and ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata, and Ovary;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC073616; AAH73616.1; -.
 DR GO; GO:0004437; F:inositol or phosphatidylinositol phosphatas. . .; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPPc.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR SMART; SM00128; IPPc; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 FT NON_TER 1 1
 SQ SEQUENCE 496 AA; 56894 MW; 832B0717978C7D63 CRC64;

Query Match 55.2%; Score 1115; DB 2; Length 496;
 Best Local Similarity 53.1%; Pred. No. 1.9e-87;
 Matches 203; Conservative 65; Mismatches 100; Indels 14; Gaps 3;

Qy 1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNKGGVNICL 60
 ||:|:| :|:| :|:|:| | | |:|:|:| : | ||||| | : :
 Db 112 MDILAPHGYVKLSSIRLQGLLLLTfVKHQHIPFVQDIRTNYIRTGLFGYWGNKGGVTVRM 171

 Qy 61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
 :|: : :|:| | : | ||: |:|:| : : : ||||| : ||:| |
 Db 172 SVYGHMICFMNCHLPAHMENTNQRLDDFERMLDTQQFDDNTGNILDHDLVFCFGDLNFR 231

 Qy 121 IEDFGLHFVRESIKNRCYGGWLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
 | |||:|:|:| : | |||||:| | : |: | | | |||||:|:| |
 Db 232 ITDFGIHFIREAINSNNKYNLLWEKDQLNIAKKKEQFLQGFLEGPLKFKPTYKFDQNSDVY 291

 Qy 181 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHF----SLSLRGYSSHMTYGISDHK 236
 ||| ||||| | | :| | | :|| |:|:|:| |
 Db 202 DTSSKKRKPAWTDRLWKLK--DVSGSDPGETTGSDFEFLKVSLDKYTSMSYGISDHK 349

 Qy 237 PVSGETFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGLRD 296
 ||:| | |:|:| : | : | | :| :|:| | | | | | | :| |
 Db 350 PVTGTFTLQKPLILTPSVTLKPEGEWNADHDSLISYSVAKDFPSSTWDWIGLYRVGFRH 409

 Qy 297 VNDYVSYAWVGDSKVSCLNQLNQVYIDISNIPTTEDEFLCYYSNSLSRSVVGISRPFQIP 356

```

      ||||:|||| |::| |:: ||||: :|| | ||||: :||: : |||:||||
Db      410 TNDYVITYAWVKDDEISFSEDCNQVYMNADDIPLDGGEFLLCYHCHNLQCLAGISQPFQIR 469

Qy      357 PG-----SLREDPLGEAQP 370
      ||      || | |
Db      470 PGRNLGLKEENRESPFKTESP 491

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RESULT 4

P5PA_MOUSE

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ID      P5PA_MOUSE      STANDARD;      PRT; 1003 AA.
AC      P59644;
DT      10-OCT-2003 (Rel. 42, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Phosphatidylinositol 4,5-bisphosphate 5-phosphatase A (EC 3.1.3.56).
GN      Name=Pib5pa;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX      MEDLINE=22354603; PubMed=12466851; DOI=10.1038/nature01266;
RA      Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA      Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA      Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA      Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA      Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA      Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA      Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA      Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA      Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA      Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA      Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA      Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA      Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA      Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA      Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA      Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA      Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA      Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA      Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA      Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA      Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA      Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA      Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA      Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA      Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA      Birney E., Hayashizaki Y.;
RT      "Analysis of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs.";
RL      Nature 420:563-573(2002).
RN      [2]
RP      SUBCELLULAR LOCATION, AND IDENTIFICATION OF DOMAIN REQUIRED FOR
RP      MEMBRANE RUFFLE LOCALIZATION.

```


RX MEDLINE=22538472; PubMed=12536145; DOI=10.1074/jbc.M209991200;
 RA Gurung R., Tan A., Ooms L.M., McGrath M.J., Huysmans R.D.,
 RA Munday A.D., Prescott M., Whisstock J.C., Mitchell C.A.;
 RT "Identification of a novel domain in two mammalian inositol-
 RT polyphosphate 5-phosphatases that mediates membrane ruffle
 RT localization. The inositol 5-phosphatase SKIP localizes to the
 RT endoplasmic reticulum and translocates to membrane ruffles following
 RT epidermal growth factor stimulation.";
 RL J. Biol. Chem. 278:11376-11385(2003).
 CC -!- FUNCTION: Inositol 5-phosphatase, which converts inositol 1,4,5-
 CC trisphosphate to inositol 1,4-bisphosphate. Also converts
 CC phosphatidylinositol 4,5-bisphosphate to phosphatidylinositol 4-
 CC phosphate and inositol 1,3,4,5-tetrakisphosphate to inositol
 CC 1,3,4-trisphosphate in vitro. May be involved in modulation of the
 CC function of inositol and phosphatidylinositol polyphosphate-
 CC binding proteins that are present at membranes ruffles (By
 CC similarity).
 CC -!- CATALYTIC ACTIVITY: D-myo-inositol 1,4,5-trisphosphate + H(2)O =
 CC myo-inositol 1,4-bisphosphate + phosphate.
 CC -!- CATALYTIC ACTIVITY: 1D-myo-inositol 1,3,4,5-tetrakisphosphate +
 CC H(2)O = 1D-myo-inositol 1,3,4-trisphosphate + phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; predominantly localized to
 CC membrane ruffles.
 CC -!- DOMAIN: The 5 Arg-Ser-Xaa-Ser-Xaa-Xaa (RSXSXX) motifs may
 CC constitute binding sites for the 14-3-3 protein.
 CC -!- PTM: Phosphorylated at Ser/Thr residues (By similarity).
 CC -!- SIMILARITY: Belongs to the inositol-1,4,5-trisphosphate 5-
 CC phosphatase type II family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR ENBL; AK034272; BAC28654.1; -.
 DR HSP; O43001; I19Z.
 DR MGD; MGI:2158663; Pib5pa.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPPc.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR SMART; SM00128; IPPc; 1.
 KW Hydrolase; Phosphorylation; Repeat; SH3-binding.
 FT DOMAIN 422 725 Catalytic (Potential).
 FT DOMAIN 726 837 Required for ruffle localization.
 FT DOMAIN 50 374 Pro-rich.
 FT DOMAIN 837 934 Ser-rich.
 FT SITE 6 11 RSXSXX motif 1.
 FT SITE 351 356 RSXSXX motif 2.
 FT SITE 871 876 RSXSXX motif 3.
 FT SITE 882 887 RSXSXX motif 4.
 FT SITE 908 913 RSXSXX motif 5.
 FT SITE 346 351 SH3-binding (Potential).
 SQ SEQUENCE 1003 AA; 107602 MW; AFF4FD929CFCB6BA CRC64;

Query Match 43.2%; Score 873.5; DB 1; Length 1003;
 Best Local Similarity 47.5%; Pred. No. 3.3e-66;
 Matches 169; Conservative 56; Mismatches 126; Indels 5; Gaps 4;

```

Qy      1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 60
      || | | :|: || |||||:|:|||| |||::: | | ||| |||||:|: |
Db      485 MDALGPFNFVLVSTVRMQGVILLLLFAKYYHLPFLRDVQTDCTRTGLGGYWGNGGGVSVRL 544

Qy      61 KLYGYYVSIINCHLPPHISNNYQRLEHFDRIEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
      :|: : :||| | | : || :| | | :| | |||||: |||:| |
Db      545 AAFGHMLCFLNCHLPAHMDKAEQRKDNFQTILSLQQFQGPAGHGILDHDLVFWFGDLNFR 604

Qy      121 IEDFGLHFVRESIKNRCYGGGLWEKDQLSIKKHDPLLREFQEGRLLPPTYKFDRNSNDY 180
      || : ||||: :| : |||||:| | | :|: ||| | | | :| | :| |
Db      605 IESYDLHFVKFAIDSNQLHQLWEKDQLNMAKNTWPILKGFQEGPLNFAPTFKFDVGTNKY 664

Qy      181 DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPV 239
      ||| ||||| |||||:| | || :| || :| ||| | :||| | :
Db      665 DTSAKRKPAWTDRLWKVK-APSGGP-SPSGRESHRLQVTQHSYRSHMEYTVSDHKPVA 722

Qy      240 GTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVND 299
      | | : ||: | | | :| | : | | |||||:| | | |
Db      723 AQFILQFAFRDDVPLVRLEVADEWARPEQAVVRYRVETVFARSSWDWIGLYRVGFRHCKD 782

Qy      300 YVSYAWVGDSKVS CSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQI 355
      ||:| | :| | :| || :| :| :| | | :|:| :|:| | |
Db      733 YVAYVWAKHEEV--DGNIYQVTFSEESLPKGHGDFILGYYSHHHSILIGVTEPFQI 836
  
```

RESULT 5

P5PA_RAT

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ID   P5PA_RAT          STANDARD;          FRT;   1001 AA.
AC   Q9JMC1;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Phosphatidylinositol 4,5-bisphosphate 5-phosphatase A (EC 3.1.3.56)
DE   (Proline-rich inositol polyphosphate 5-phosphatase).
GN   Name=Pib5pa; Synonyms=Pipp;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND
RP   ENZYMATIC ACTIVITY.
RC   TISSUE=Brain;
RX   MEDLINE=20062911; PubMed=10593988; DOI=10.1074/jbc.274.51.36790;
RA   Mochizuki Y., Takenawa T.;
RT   "Novel inositol polyphosphate 5-phosphatase localizes at membrane
RT   ruffles.";
RI   J. Biol. Chem. 274:36790-36795(1999).
CC   -!- FUNCTION: Inositol 5-phosphatase, which converts inositol 1,4,5-
CC   trisphosphate to inositol 1,4-bisphosphate. Also converts
CC   phosphatidylinositol 4,5-bisphosphate to phosphatidylinositol 4-
CC   phosphate and inositol 1,3,4,5-tetrakisphosphate to inositol
CC   1,3,4-trisphosphate in vitro. May be involved in modulation of the
  
```

CC function of inositol and phosphatidylinositol polyphosphate-
 CC binding proteins that are present at membranes ruffles.
 CC -!- CATALYTIC ACTIVITY: D-myo-inositol 1,4,5-trisphosphate + H(2)O =
 CC myo-inositol 1,4-bisphosphate + phosphate.
 CC -!- CATALYTIC ACTIVITY: 1D-myo-inositol 1,3,4,5-tetrakisphosphate +
 CC H(2)O = 1D-myo-inositol 1,3,4-trisphosphate + phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; predominantly localized to
 CC membrane ruffles.
 CC -!- TISSUE SPECIFICITY: Expressed in heart, brain, kidney, stomach,
 CC small intestine and lung. Not expressed in spleen, thymus,
 CC skeletal muscle, testis and skin.
 CC -!- DOMAIN: The 5 Arg-Ser-Xaa-Ser-Xaa-Xaa (RSXSXX) motifs may
 CC constitute binding sites for the 14-3-3 protein.
 CC -!- PTM: Phosphorylated on Ser/Thr residues.
 CC -!- SIMILARITY: Belongs to the inositol-1,4,5-trisphosphate 5-
 CC phosphatase type II family.
 CC -----
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 CC -----
 DR EMBL; AB032551; BAA90553.1; -.
 DR HSSP; O43001; 1I9Z.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPPc.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR SMART; SM00128; IPPc; 1.
 KW Hydrolase; Phosphorylation; Repeat; SH3-binding.
 FT DOMAIN 420 723 Catalytic (Potential).
 FT DOMAIN 724 835 Required for ruffle localization (By
 FT similarity).
 FT DOMAIN 50 387 Pro-rich.
 FT DOMAIN 835 932 Ser-rich.
 FT SITE 6 11 RSXSXX motif 1.
 FT SITE 351 356 RSXSXX motif 2.
 FT SITE 869 874 RSXSXX motif 3.
 FT SITE 880 885 RSXSXX motif 4.
 FT SITE 906 911 RSXSXX motif 5.
 FT SITE 346 351 SH3-binding (Potential).
 SQ SEQUENCE 1001 AA; 107207 MW; 7BE7741FEF8F3FAB CRC64;

Query Match 43.2%; Score 872.5; DB 1; Length 1001;
 Best Local Similarity 47.5%; Pred. No. 4e-66;
 Matches 169; Conservative 56; Mismatches 126; Indels 5; Gaps 4;

Qy 1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGKGVNICL 60
 || || :|: || |||||:|:|:| |||:|: | ||| |||||:|:|
 Db 483 MDALGPFNFVLVSTVRMQGVILLVFAKYHLPFLRDVQTDCTRTGLGGYWGNGKGVSVRL 542
 Qy 61 KLYGYVYSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR 120
 :|: : :| ||| | : || :| || :| |||||: |||:|
 Db 543 AAFGHMLCFLNCHLPAHMDKAEQRKDNFQTILSLQQFQGPAGHILDHDLVFWFGDLNFR 602

Qy 121 IEDFGLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLFPPTYKFDRNSNDY 180
 || : ||||: :| : |||||::|| |:: ||| | | ||: || | :| |
 Db 603 IESYDLHFVKFAIDSNQLHQLWEKDQLNMAKNTWPIKGFQEGPLNFAPTFKFDVGTNKY 662

Qy 181 DTSEKKRKPAWTDRLWRLKRQPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPV 239
 ||| ||||| |||||::| | || :| || :| ||| | :||| ||:|
 Db 663 DTSKKRKPAWTDRLWKVK-APSGGP-SPSGRESHRLQVTQHSYRSHMEYTVSDHKPVA 720

Qy 240 GTFDLELKLPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVND 299
 | |: ||: | | | :| | :| | |||||: || | |
 Db 721 ARFLQLQAFRDDVPLVRLEVADEWARPEQAVVRYRVETVFARSSWDWIGLYRVGFRHCKD 780

Qy 300 YVSYAWVGDSKVSCLNQLNQYIDISNIPTTEDEFLLCYYSNSLRVVGISRPFQI 355
 ||:| | :| | :| | :| | :| | ||: :|:: |||
 Db 781 YVAYVWAKHEEV--DGNIIYQVTFSEESLPKGGHDFILGYSSHHSILIGVTEPFQI 834

RESULT 6

Q6ZTH6

ID Q6ZTH6 PRELIMINARY; PRT; 638 AA.
 AC Q6ZTH6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein FLJ44647.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum;
 RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
 RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
 RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
 RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
 RA Masuho Y., Nagai K., Isogai T.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK126610; BAC86611.1; -.
 DR GO; GO:0004437; F:inositol or phosphatidylinositol phosphatas. . .; IEA.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPPc.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR SMART; SM00128; IPPc; 1.
 SQ SEQUENCE 638 AA; 70211 MW; EE7EBE8F0960D28C CRC64;

Query Match 43.1%; Score 870.5; DB 2; Length 638;
 Best Local Similarity 47.8%; Pred. No. 3.3e-66;
 Matches 170; Conservative 54; Mismatches 127; Indels 5; Gaps 4;

Qy 1 MDVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICL 60
 || | | :|: || |||||::||: ||| ||||| |||||: |||
 Db 120 MDALGPPNFVFLVSSVRMQGVILLLVFAKYHLPFLRDVQTDCTRTGLGGYWGNGGGVSVRL 179

| | | | |
|----|-----|--|-----|
| Qy | 61 | KLYGYVSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 120 |
| Db | 180 | AAFGHMLCFLNCHLPAHMDKAEQRKDNFQTILSLQQFQGGPAQGILDHDLVFWFGDLNFR | 239 |
| Qy | 121 | IEDFGLHFVRESIKNRCYGGLEWKDQLSIAKKHDPLLREFQEGRLLPPTYKFDRNSNDY | 180 |
| Db | 240 | IESYDLHFVKFAIDSDQLHQLWEKDQLNMAKNTWPILKGFQEGPLNFAPTFKFDAGTNKY | 299 |
| Qy | 181 | DTSEKKRKPAWTDRIWLRLKRPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPVS | 239 |
| Db | 300 | DTSAKRKPAWTDRIWLKVK-APGGGP-SPSGRKSHRLQVTQHSYRSHMEYTVSDHKPVA | 357 |
| Qy | 240 | GTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSTSDFPSSPWDWIGLYKVGLRDVND | 299 |
| Db | 358 | AQFLQFAFRDDMPLVRLEVADEWVRPEQAVVRYRMETVFARSSWDWIGLYRVGFRHCKD | 417 |
| Qy | 300 | YVSYAWVGDSKVS CSDN LNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFQI | 355 |
| Db | 418 | YVAYVWAKHEDV--DGNTYOVTFSEESLPKGHGDFILGYYSNHHSILIGITEPFOI | 471 |

PEPA HUMAN

ID P5PA HUMAN STANDARD; PRT; 1006 AA.

AC 015735; 08N902; 09UDT9;

DT' 10-OCT-2003 (Rel. 42, Created)

D2 10-CCT-2003 (Rel. 42, Last sequence update)

DT 95-JUL-2004 (Rel. 44, Last annotation update)

DE Phosphatidylinositol 4,5-bisphosphate 5-phosphatase A (EC 3.1.3.56):

GN Name=PIB5PA; Synonyms=PIPP;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OK NBI TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Heart;

RX PubMed=14702039; DOI=10.1038/nq1285;

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.

RA: Nagahari K., Murakami K., Yasuda T., Iwavanagi T., Wagatsuma M.

BA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.

BA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.

BA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.

RA Yamazaki M Nipomiya K Ishibashi T Yamashita H Murakawa K

RA Fujimori K Tanai H Kimata M Watanabe M Hiraoka S Chiba Y

RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba T.
PA Ishida S Ono Y Takiguchi S Watanabe S Yosida M Hotuta T

RA Kusano, I. Kanehori, K. Takahashi-Fujii, A. Hara, H. Tanase, T. O.

RA Kutsano S., Kamenohi K., Takamashi-Fujii A., Hara H., Iinase I.
 RA Nomura Y, Togiya S, Komai F, Hara R, Takeuchi K, Arita M

RA Imose N, Musashino K, Yuuki H, Oshima A, Sasaki N, Aotsuka S

RA Imose N., Musashino K., Yuuki H., Ushima A., Sasaki N., Aotsuki
BA Yoshikawa Y, Matsunawa H, Ichihara T, Shiohata N, Sano S

RA Yoshikawa Y., Matsunawa H., Ichihara I., Shionata N., Sano S.,
RA Moriya S., Moriyama H., Satoh N., Takami S., Terashima Y., Suzuki O.

RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.
RA Nakagawa S., Sano A., Mizoguchi H., Goto Y., Shimizu E., Wakabe H.

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami R.

RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami
 RA Yonasaki M., Watanabe K., Kumagai J., Itakura S., Fukumura Y.

RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
 RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
 RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Laversha M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
 RA McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Scderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
 RA Schcet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
 RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
 RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
 RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
 RA Khan A.S., Lane L., Tilahun Y., Wright H.;
 RT "The DNA sequence of human chromosome 22."

RL Nature 402:489-495(1999).
 RN [3]
 RP SEQUENCE OF 648-1044 FROM N.A.
 RC TISSUE=Brain;
 RA Nussbaum R.L.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Inositol 5-phosphatase, which converts inositol 1,4,5-
 CC trisphosphate to inositol 1,4-bisphosphate. Also converts
 CC phosphatidylinositol 4,5-bisphosphate to phosphatidylinositol 4-
 CC phosphate and inositol 1,3,4,5-tetrakisphosphate to inositol
 CC 1,3,4-trisphosphate in vitro. May be involved in modulation of the
 CC function of inositol and phosphatidylinositol polyphosphate-
 CC binding proteins that are present at membranes ruffles (By
 CC similarity).
 CC -!- CATALYTIC ACTIVITY: D-myo-inositol 1,4,5-trisphosphate + H(2)O =
 CC myo-inositol 1,4-bisphosphate + phosphate.
 CC -!- CATALYTIC ACTIVITY: 1D-myo-inositol 1,3,4,5-tetrakisphosphate +
 CC H(2)O = 1D-myo-inositol 1,3,4-trisphosphate + phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; predominantly localized to
 CC membrane ruffles (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q15735-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q15735-2; Sequence=VSP_007296;
 CC -!- DOMAIN: The 5 Arg-Ser-Xaa-Ser-Xaa-Xaa (RSXSXX) motifs may
 CC constitute binding sites for the 14-3-3 protein.
 CC -!- PTM: Phosphorylated at Ser/Thr residues (By similarity).
 CC -!- SIMILARITY: Belongs to the inositol-1,4,5-trisphosphate 5-
 CC phosphatase type II family.
 CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AK095944; BAC04657.1; -.
 DR EMBL; AC005005; AAD15618.1; ALT_SEQ.
 DR EMBL; U45975; AAB03216.1; -.
 DR HSSP; O43001; 1I9Z.
 DR Genew; HGNC:8956; PIB5PA.
 DR MIM; 606481; -.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPPc.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR SMART; SM00128; IPPc; 1.
 KW Alternative splicing; Hydrolase; Phosphorylation; Repeat; SH3-binding.
 FT DOMAIN 425 728 Catalytic (Potential).
 FT DOMAIN 729 840 Required for ruffle localization (By
 FT similarity).
 FT DOMAIN 122 371 Pro-rich.

| | | | | |
|----|----------|----------|------------|--------------------------|
| FT | DOMAIN | 840 | 937 | Ser-rich. |
| FT | SITE | 102 | 107 | RSXSXX motif 1. |
| FT | SITE | 350 | 355 | RSXSXX motif 2. |
| FT | SITE | 874 | 879 | RSXSXX motif 3. |
| FT | SITE | 885 | 890 | RSXSXX motif 4. |
| FT | SITE | 911 | 916 | RSXSXX motif 5. |
| FT | SITE | 345 | 350 | SH3-binding (Potential). |
| FT | VARSPLIC | 1 | 367 | Missing (in isoform 2). |
| FT | | | | /FTId=VSP_007296. |
| FT | CONFLICT | 596 | 596 | E -> D (in Ref. 1). |
| FT | CONFLICT | 610 | 612 | SYD -> ARG (in Ref. 3). |
| SQ | SEQUENCE | 1006 AA; | 107210 MW; | DCFDD67F464C6E5D CRC64; |

| | | | |
|----|-----|---|-----|
| Qy | 1 | MDVLSPLSFIFIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGKGGVNICL | 60 |
| Db | 438 | MDALGPPNFVFLVSSVRMQGVILLVFAKYHLPFLRDVQTDCTRTGLGGYWGNGKGGVSVRL | 547 |
| Qy | 61 | KLYGYVYSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFR | 120 |
| Db | 546 | AAFGHMLCFLNCHLPAHMDKAEQRKDNFQTILSLQQFQGPQAQGILDHELVFWFGDLNFR | 607 |
| Qy | 121 | IEDFGLHFVRESIKNRCYGGGLEWKDQLSIAKKHDPLLREFQEGRLFPPTYKFDRNSNDY | 180 |
| Db | 609 | IESYDLHFVKFAIDSDQLHQLWEKDQLNMAKNTPWILKGFQEGPLNFAPTFKFEVGTNKY | 667 |
| Qy | 261 | DTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASH-FSLSLRGYSSHMTYGISDHKPV | 239 |
| Db | 658 | DTSAKKRKPAWTDRLWKVK-APGGGP-SPSGRKSHRLQVTQHSYRSHMEYTVSDHKPVA | 725 |
| Qy | 340 | GTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTDFPSSPWDWIGLYKVGLRDVND | 299 |
| Db | 726 | AQFLQQAFRDDMPLVRLEVADEWVRPEQAVVRYRMETVFARSSWDWIGLYRVGFRHCKD | 785 |
| Qy | 300 | YVSYAWVGDSKVSCSDNLNQVYIDISNIPTTEDEFLLCYYSNSLRSVVGISRPFI | 355 |
| Db | 786 | YVAYVWAKHEDV--DGNTYQVTFSEESLPKGHGDFILGYSHNHSILIGITEPFI | 839 |

RESULT 8

```
ID      Q7PYY6      PRELIMINARY;      PRT;      501 AA.
AC      Q7FY76;
DT      01-MAR-2004 (TrEMBLrel. 26, Created)
DT      01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      AgCP9655 (Fragment).
GN      Name=agCG49651; ORFNames=ENSANGG00000016677;
OS      Anopheles gambiae str. PEST.
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX      NCBI_TaxID=180454;
RN      [1]
RP      SEQUENCE FROM N.A.
```


RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008986; EAA00417.1; -.
DR HSSP; O43001; 1I9Z.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
FT NON_TER 1 1
SQ SEQUENCE 501 AA; 57809 MW; F8C7DFBBF38FCA79 CRC64;

Query Match 25.5%; Score 516; DB 2; Length 501;
Best Local Similarity 30.7%; Pred. No. 9e-36;
Matches 116; Conservative 70; Mismatches 152; Indels 40; Gaps 7;

Qy 2 DVLSPLSFIKVSHVRMQGILLLVFAKYQHLPYIQLSTKSTPTGLFGYWGNGKGVNICKL 61
: || : : : ||| : || || : || : : : | : | || | || || | : | :
Db 127 EVLKERDYVVIKTEQMQLLLSVFARRKHLHLRQVETETRTGLGGIWNKGAVSIRMN 186
Qy 62 LYGYYSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFRI 121
: || : : : || | : : : : || : : : | : | || : ||| : ||| :
Db 137 VYGSSICLVNAHLAAHDMLEERINDYERIVQEQKFHV KAKETIFDHDYVFWFGDLNFRL 246
Qy 122 -----EDFGLHFVRESIKNRCYGLWEKDQLSIAKKHDPLLREFQEGRLLPPTYKF 173
: : : : | : : | ||| : : : : : | : ||| : ||| :
Db 247 TGEATTSAD EIRAMVARDELKQ-----LIEKDQLLLVRREGRAFAQLQERLPQFPPTFKF 301
Qy 174 DRNSNDYDTSEKKRKPATWDRILWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGIS 233
: || : || : ||| ||| ||| : : : : : | : || : ||
Db 302 EHGSNEYD---MKRRPAWTDRI LYAVNENNYRN-----VRLTAEQTSYKSHPSYSIS 350
Qy 234 DHKPVSGTFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVG 293
||| : | : : : : : | : | : : | : ||| : :
Db 351 DHKPVTS EFTLVKYEDTTERTVSFKPIELWLVGEPNTIEYVIPNGFEEGNADWIGIYREN 410
Qy 294 LRDVNDYVSYAW-----VGDSKVSCSDNLNQVYIDIS---NIPTTEDEFLLCYYS 340
: : : : : : : : : : | : | : : | : | :
Db 411 FTSLS EYLAYEYETETKDKQHQLNEQQLQHMQNTRTVQLTFSENVSLPLGTRYQLLYFQS 470
Qy 341 NSLRSV---VGISRPFQI 355
| | ||| | :
Db 471 TGTRGV TGLVGISPAFAV 488

RESULT 9

Q9VXE7

ID Q9VXE7 PRELIMINARY; PRT; 508 AA.
AC Q9VXE7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CG9784-PA (SD21513p).
GN ORFNames=CG9784;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDRJ databases.
 DR EMBL; AE003502; PAF48627.1; -.
 DR EMBL; AY119249; AAM51109.1; -.
 DR HSSP; Q43001; 1I9Z.
 DR EntAct; Q9VXE7; -.
 DR FlyBase; FBgn0030761; CG9784.
 DR CO; GO:0004437; F:inositol or phosphatidylinositol phosphatas. . .; IEA.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPPc.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR SMART; SM00128; IPPc; 1.
 SQ SEQUENCE 508 AA; 58973 MW; F7008010B55AD722 CRC64;

Query Match 25.1%; Score 507.3; DB 2; Length 508;
 Best Local Similarity 34.3%; Pred. No. 5e-35;
 Matches 111; Conservative 62; Mismatches 130; Indels 21; Gaps 7;

QY 2 DVLSPLSFIKVS HVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGKGVNICKL 61
 ::| ::| :|||:| :| :||: ::| : :| || | ||||| |::
 Db 106 ELLRNYDYVAVKTEQMQLLLSMFVRRQHVEHLQDIEAEFTRTGFGGIWGNKGA VSVRFT 165

Qy 62 LYGYYSIINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIPNILDHDLIIWFGDMNFRI 121
 ||| :: : || | :|| : :|| : : | ||| : ||||:| ||:
 Db 166 LYGCGLAFVVAHLTAHDHMMDERIEDYKQILENHHYHVKRYREIYDHDYVFWFGDLNFR 225

Qy 122 E--DFGLHFVRESIKNRC-YGGLWEKDQL-SIAKKHDPLLREFQEGRLLPPTYKFDRNS 177
 : | ||| :: : | :||| : :| : || ||||:| | :
 Db 226 QGSDSSTE-VRELVRDESQHEALIQRDQLYQVREKSQLAFQVLQERLPAPFPPTFKFREGT 284

Qy 178 NDYDTSEKKRKPATDRILWR---LKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISD 234
 ::|| ||:|||||:: | || | : | || | |||
 Db 285 SEYDL---KRRPAWTDRIYAVQPLNRQ-----PGMQLSIEQCSYKSHPLYTISD 331

Qy 235 HKPVSFTDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSSSTSDFPSSPWDWIGLYKVGL 294
 ||||: | :| | || :| | | : :: | | :| ||||:|
 Db 332 HKPVTSDFTIKLYPNVRAPGVVFSPLSLWKIGDENTVEYHKQAEFDEGSNDWIGIFPSEY 391

Qy 295 RDVNDYVSYAWVGDSKVSCLN 318
 : ||||: | :| :| :|
 Db 392 ASLADYVAYEYVNAESPSSSDSN 415

RESULT 10

Q9V7X0

ID Q9V7X0 PRELIMINARY; PRT; 357 AA.
 AC Q9V7X0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created).
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE CG6805-PA (LD06095p).
 GN CRFNames=CG6805;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Eceson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;

RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;

RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [5]

RP SEQUENCE FROM N.A.

RG FlyBase;

RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenvong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE003804; AAF57919.1; -.
 DR EMBL; AY069356; AAL39501.1; -.
 DR HSSP; O43001; 1I9Z.
 DR IntAct; Q9V7X0; -.
 DR FlyBase; FBgn0034179; CG6805.
 DR GO; GO:0004437; F:inositol or phosphatidylinositol phosphatas. . .; IEA.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPPc.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR SMART; SM00128; IPPc; 1.
 SQ SEQUENCE 357 AA; 40497 MW; 586C3CD3E7F8BA28 CRC64;

Query Match 22.8%; Score 460.5; DB 2; Length 357;
 Best Local Similarity 34.0%; Pred. No. 3.5e-31;
 Matches 104; Conservative 60; Mismatches 105; Indels 37; Gaps 6;

Qy 2 DVLSPLSFIKVS HVRMQ GILL LVFAKYQHLPYIQILSTKSTPTGLFCGYWGNKGGVNICKL 61
 | | | | : | | : : | | | : : | | : : | : : | : | : | | | | : | |
 Db 73 DSLSDHQFVKVDSKQLQGILITMFAQHKH I PHMKEIETEATRTGLGGLWGNKGA VSIRLS 137

 Qy 62 LYGYYVSIINCHLPPHISNNYQRLEHFDRILEMQNCGRDIPNILDHDLIIWFGDMNFRI 121
 | | | | : : | | | : : | | : : | : : | : | | | : | | | : | | :
 Db 138 LYGTGVAFVCSHLAAHDEKLKERIEDYHQIVDNH KYNAQGYRRIFDHD FVFWFGDLNFRL 197

 Qy 122 E-DFGLHFVRESIKNRCYGG LWEKDQLSIAKKHDPLLREFQEGRLFPPTYKFDRNSNDY 180
 | | | | : : | | | : | | | : : | : | : | | : | | : | | |
 Db 198 SGDMSAWDVRTDVENQRYADLLKLDQLNLLREKGN AFSLL EEQQPNFAPTFKFVEGTNDY 257

 Qy 181 DTSEKKRKPAWTDRI LWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSG 240
 : | | : | | | | | : : : | | | : | | | | : | | | | |
 Db 258 NL---KRRPAWCDRI LHRVQ-----SNIYPGITLSANQLSYQSHMDYTLSDHKPVSA 306

 Qy 241 TFDLELKPLVSAPLIVLMPEDLWTVENDMMVSYSS TSDFPSSPDWIGLYKVGLRDVNDY 300
 | | : : : : : | | : : | | : : | | : : | | : : | | : : |
 Db 307 TFNYKVE-----AANQTYTDEELHEMTHGSASS-PATP-----NVS 341

 Qy 301 VSYAWV 306
 : | : | : |
 Db 342 LSFAFV 347

RESULT 11
 Q86YE1

ID Q86YE1 PRELIMINARY; PRT; 736 AA.
 AC Q86YE1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE INPP5B protein (Fragment).
 GN Name=INPP5B;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteiman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC042529; AAH42529.2; -.
 DR HSSP; O43001; 1I9Z.
 DR GO; GO:0004437; F:inositol or phosphatidylinositol phosphatas. . .; IEA.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPPc.
 DR InterPro; IPR000198; RhoGAP.
 DR InterPro; IPR008936; Rho_GAP.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR Pfam; PF00620; RhoGAP; 1.
 DR SMART; SM00128; IPPc; 1.
 DR SMART; SM00324; RhoGAP; 1.
 DR PROSITE; PS50238; RHOGAP; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 736 AA; 84286 MW; ACCA05487919D1D4 CRC64;

Query Match 21.4%; Score 432.5; DB 2; Length 736;
 Best Local Similarity 37.0%; Pred. No. 2.4e-28;

Matches 90; Conservative 45; Mismatches 87; Indels 21; Gaps 4;

```
Qy      9 FIKVSHVRMQGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGGGVNICLKLYGYYS 68
      : || :|: ||: ||: | :| || : :: ||: | ||||| | : : :
Db     159 YAKVKLIRLVGIMLLLVYKQEHAAAYISEVEAETVGTGIMGRMGNGGGVAIRFQFHNTSIC 218

Qy     69 IINCHLPPHISNNYQRLEHF-DRILEMQNCE-GRDIP--NILDHDLIIWFGDMNFRIEDF 124
      ::| || || :| : : | || | : | :||:|:| ||:|:|:|
Db     219 VVNSHLAAHIEEYERRNQDYKDICSRMQFCQPDPSLPPLTISNHDVILWLGLDNLNRIEEL 278

Qy    125 GLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPDLLREFQEGRLLPPTYKFDRNSNDYDTSE 184
      : |:: |: : : |: ||| | : || | | ||||:| |:|:|
Db    279 DVEKVKKLIEEKDFQMLYAYDQLKIQVAAKTVFEGFTEGELTFQPTYKYDTGSDDWDTSSE 338

Qy    185 KKRKPAWTDRILWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSGTDFDL 244
      | | ||| ||||: | ::: | || | ||||| ||:
Db    339 KCRAPAWCDRILWKGK-----NITQLSYQSHMALKTSDHKPVSSVFDI 381

Qy    245 ELK 247
      ::
Db    382 GVR 384
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RESULT 1:

Q6PD53

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ID   Q6PD53      PRELIMINARY;      PRT;      748 AA.
AC   Q6PD53;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Inositol polyphosphate-5-phosphatase, 75kDa.
GN   Name=INPP5B;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
```


RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Director MGC Project;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: BC062317; AAH62317.1; -.
 DR GO; GO:0004437; F:inositol or phosphatidylinositol phosphatas. . .; IEA.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPPc.
 DR InterPro; IPR001220; Lectin_legB.
 DR InterPro; IPR000198; RhoGAP.
 DR InterPro; IPR008936; Rho_GAP.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR Pfam; PF00620; RhoGAP; 1.
 DR SMART; SM00128; IPPc; 1.
 DR SMART; SM00324; RhoGAP; 1.
 DR PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
 DR PROSITE; PS50238; RHOGAP; 1.
 SQ SEQUENCE 871 AA; 99120 MW; C9CF9E0430097153 CRC64;

Query Match 21.4%; Score 432.5; DB 2; Length 871;
 Best Local Similarity 37.0%; Pred. No. 3e-28;
 Matches 90; Conservative 45; Mismatches 87; Indels 21; Gaps 4;

QY 9 FIKVSHVRMQGILLLVFAKYQHLPYIQLSTKSTPTGLFGYWGNGKGGVNICLKLYGYVVS 68
 : || :|: ||:|:: | :| || : :: ||: | ||||| | : : :
 Db 336 YAKVKLIRLVGIMLLLVKQEAAYISEVEAETVGTGIMGRMGNGKGGVAIRFQFHNTSIC 395
 QY 69 IINCHLPPHISNNYQRLEHF-DRILEMQNCE-GRDIP--NILDHDLIIWFGDMNFRIEDF 124
 : :| || || :| : : | || | : | :||:|:| ||:|:|:|:
 Db 396 VVNSHLAAHIEEYERRNQDYKDICSRMQFCQPDPSLPPLTISNHDVILWLGLDNLNRIEEL 455
 QY 125 GLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLFPPTYKFDRNSNDYDTSE 184
 : |:: |: : : |: ||| | : | || | | |||:| |:|:| |||

Db 456 DVEKVKKLIEEKDFQMLYAYDQLKIQVAAKTVFEGFTEGELTFQPTYKYDTGSDDWDTSE 515

Qy 185 KKRKPAWTDRILWRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSGTFDL 244
 | | | | | | | : | : : | | | | | | | | :
 Db 516 KCRAPAWCDRILWKGK-----NITQLSYQSHMALKTSDHKPVSSVFDI 558

Qy 245 ELK 247
 : :
 Db 559 GVR 561

RESULT 14

I5P2_HUMAN

ID I5P2_HUMAN STANDARD; PRT: 942 AA.
 AC P32019;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Type II inositol-1,4,5-trisphosphate 5-phosphatase precursor
 DE (EC 3.1.3.36) (Phosphoinositide 5-phosphatase) (5PTase) (Fragment).
 CN Name=INPP5B;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95238452; PubMed=7721860; DOI=10.1074/jbc.270.16.9370;
 RA Jefferson A.B., Majerus P.W.;
 RT "Properties of type II inositol polyphosphate 5-phosphatase.";
 RL J. Biol. Chem. 270:9370-9377(1995).
 RN [2]
 RP SEQUENCE OF 233-903 FROM N.A., AND SEQUENCE OF 270-288.
 RC TISSUE=Placenta;
 RX MEDLINE=92041857; PubMed=1718960;
 RA Ross T.S., Jefferson A.B., Mitchell C.A., Majerus P.W.;
 RT "Cloning and expression of human 75-kDa inositol polyphosphate-5-
 phosphatase.";
 RL J. Biol. Chem. 266:20283-20289(1991).
 CC -!- FUNCTION: Hydrolyzes the calcium-mobilizing second messenger
 CC Ins(1,4,5)P3, this is a signal-terminating reaction.
 CC -!- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = 1-phosphatidyl-1D-myo-inositol 4-phosphate
 CC + phosphate.
 CC -!- TISSUE SPECIFICITY: Platelets.
 CC -!- SIMILARITY: Belongs to the inositol-1,4,5-trisphosphate 5-
 CC phosphatase type II family.
 CC -!- SIMILARITY: Contains 1 Rho-GAP domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; M74161; AAA79207.1; -.
 DR HSSP; O43001; 1I9Z.
 DR Genew; HGNC:6077; INPP5B.
 DR MIM; 147264; -.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0004445; F:inositol-polyphosphate 5-phosphatase activity; NAS.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR000300; IPPc.
 DR InterPro; IPR000198; RhoGAP.
 DR InterPro; IPR008936; Rho_GAP.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR Pfam; PF00620; RhoGAP; 1.
 DR SMART; SM00128; IPPc; 1.
 DR SMART; SM00324; RhoGAP; 1.
 DR PROSITE; PS50238; RHOGAP; 1.
 KW Direct protein sequencing; Hydrolase.
 FT NON_TER 1 1
 FT PROPEP <1 269
 FT CHAIN 270 942 Type II inositol-1,4,5-trisphosphate 5-phosphatase.
 FT DOMAIN 770 942 Rho-GAP.
 FT CONFLICT 536 555 GSDDWDTSEKCRAPAWCDRI -> RALTTGIPVRSVALLPG
 FT VIGF (in Ref. 2).
 FT CONFLICT 860 860 G -> P (in Ref. 2).
 SQ SEQUENCE 942 AA; 106614 MW; 416F9F934E450923 CRC64;

Query Match 21.4%; Score 432.5; DB 1; Length 942;
 Best local Similarity 37.0%; Pred. No. 3.3e-28;
 Matches 90; Conservative 45; Mismatches 87; Indels 21; Gaps 4;

QY 9 FIKVSHVRMQGILLLVFAKYQHLPIYIQLSTKSTPTGLFGYWGNGGGVNICLKLYGYVVS 68
 : || :|: ||:|:|:| :| || : :| :| ||||| | : : :
 Db 365 YAKVKLIRLVGIMLLLYVKQEHAAYISEVEAETVGTGIMGRMGNGGGVAIRFQFHNTSIC 424
 QY 69 IINCHLPPHISNNYQRLEHF-DRILEMQNCE-GRDIP--NILDHDLIIWFGDMNFRIEDF 124
 :| || || :| : :| || | :| | :||:|:| ||:|:|:|:
 Db 425 VVNSHLAAHIEEYERRNQDYKDICSRMQFCQPDPSLPPLTISNHDVILWLGLDLYRIEEL 484
 QY 125 GLHFVRESIKNRCYGGWLEKDQLSIKKHDPLLREFQEGRLLPPTYKFDRNSNDYDTSE 184
 : |:: |: : : |: ||| | : | ||| | ||||:| |:|:|:|:
 Db 485 DVEKVKKLIEEKDFQMLYAYDQLKIQVAAKTVFEGFTEGELTFQPTYKYDTGSDDWDTSE 544
 QY 185 KKRKPAWTDRLWLKRPQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVSGTFDL 244
 | | ||| ||||:| ::: | ||| ||||| ||:
 Db 545 KCRAPAWCDRILWK GK-----NITQLSYQSHMALKTSDHKPVSSVFDI 587
 QY 245 ELK 247
 : :
 Db 588 GVR 590

RESULT 15

Q8CF65

ID Q8CF65 PRELIMINARY; PRT; 742 AA.
 AC Q8CF65;
 DT C1-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
 DE clone:1200004L23 product:inositol polyphosphate-5-phosphatase, 75 kDa,
 DE full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.;

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RA Arakawa T., Arono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
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DR EMBL; AK004601; BAC25089.1; -.
DR HSSP; O43001; 1I9Z.
DR GO; GO:0004437; F:inositol or phosphatidylinositol phosphatas. . .; IEA.
DR InterPro; IPR005135; Exo_endo_phos.
DR InterPro; IPR000300; IPPc.
DR InterPro; IPR000198; RhoGAP.
DR InterPro; IPR008936; Rho_GAP.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR SMART; SM00128; IPPc; 1.
DR SMART; SM00324; RhoGAP; 1.
DR PROSITE; PS50238; RHOGAP; 1.
SQ SEQUENCE 742 AA; 84871 MW; A25751E2A3C40404 CRC64;

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| Qy | 9 | FIKVSHVVRMQGIGILLLVFAKYQHLPYIQILSTKSTPTGLFGYWGNGKGGVNICLKLYGYIYVS | 68 |
|----|-----|---|-----|
| Db | 165 | YAKVKFVRLVVGIMLLLVYKQEHAAIYSEVEAETVGTGIMGRMGNGKGGVAIRFQLHNTSIC | 224 |
| Qy | 69 | IINCHLPPHISNNYQRLEHFDRILEMQNCEGRDIP-----NILDHDLIIWFGDMNF | 119 |
| Db | 225 | VVNSHLAAHTEEYERRNQDYRDI-----CSRMQFPQVDPSQPPLTINKHDVILWLGDLNY | 279 |
| Qy | 120 | RIEDFGLHFVRESIKNRCYGGGLWEKDQLSIAKKHDPDLLREFQEGRLLFPPTYKFDNRNSND | 179 |
| Db | 280 | RIEELDVGKVKKLVEEKAFQTLYAHDQLKIQVAARTIFDGFTEGEITFQPTYKYDTGSDD | 339 |
| Qy | 180 | YDTSEKKRKPAWTDRLWLRLKRQPCAGPDTPIPPASHFSLSLRGYSSHMTYGISDHKPVS | 239 |
| Db | 340 | WDTSEKCRAPAWCDRLWKKGK-----NITQLSYQSHMALKTSDHKPVS | 382 |
| Qy | 240 | GTFDLELK | 247 |
| Db | 383 | SVFDIGVR | 390 |